

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 16:33:30; Search time 3423 Seconds

(without alignments)
15968.534 Million cell updates/sec

Title: US-10-602-166-2

Perfect score: 1436

Sequence: 1 cattcagaatcatctccagc.....tatcaagggtggtaaacctgg 1436

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

C	31	88.4	6.4	280	6	C71788
C	26	91.2	6.4	642	8	AQ578656
C	27	90.2	6.3	624	9	CL790230
C	28	90.2	6.3	640	9	CL749019
C	29	90.2	6.3	774	9	CL612072
C	30	90	6.3	562	9	CL629198
C	31	88.4	6.2	754	8	AQ840531
C	32	86.2	6.0	699	9	CL858276
C	33	86.2	6.0	773	9	CL736927
C	34	86	6.0	742	9	CL627803
C	35	84.6	5.9	738	9	CL753761
C	36	83.2	5.8	789	9	CL768364
C	37	82.8	5.8	621	9	CW538474
C	38	82.6	5.8	617	9	AG211983
C	40	81.2	5.7	745	9	CL853543
C	41	81	5.6	336	9	CL838261
C	42	81	5.6	576	9	AG212556
C	43	80.6	5.6	756	9	CL859905
C	44	80	5.6	677	9	CL772037
C	45	80	5.6	490	9	AB156569
				685	9	AG021430

C	25	91.4	6.4	280	6	C71788
C	26	91.2	6.4	642	8	AQ578656
C	27	90.2	6.3	624	9	CL790230
C	28	90.2	6.3	640	9	CL749019
C	29	90.2	6.3	774	9	CL612072
C	30	90	6.3	562	9	CL629198
C	31	88.4	6.2	754	8	AQ840531
C	32	86.2	6.0	699	9	CL858276
C	33	86.2	6.0	773	9	CL736927
C	34	86	6.0	742	9	CL627803
C	35	84.6	5.9	738	9	CL753761
C	36	83.2	5.8	789	9	CL768364
C	37	82.8	5.8	621	9	CW538474
C	38	82.6	5.8	617	9	AG211983
C	40	81.2	5.7	745	9	CL853543
C	41	81	5.6	336	9	CL838261
C	42	81	5.6	576	9	AG212556
C	43	80.6	5.6	756	9	CL859905
C	44	80	5.6	677	9	CL772037
C	45	80	5.6	490	9	AB156569
				685	9	AG021430

RESULT	1	CL921501/c	CL921501	CL921501	376 bp	DNA
DEFINITION		OA_ABA0026D24.r	OA_ABA	Oryza australiensis	genomic clone	GSS
LOCUS		OA_ABA0026D24	3'	genomic survey sequence.		
VERSION		CL921501	1	GI:52037176		
KEYWORDS		GSS.				
SOURCE		Oryza				
ORGANISM		Oryza australiensis				
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
REFERENCE	1	(bases 1 to 376)				
AUTHORS	Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.					
TITLE	OMAP Project					
JOURNAL	Unpublished (2004)					
COMMENT	Contact: Rod A. Wing					
	Arizona Genomics Institute					
	University of Arizona					
	Forbes Building Room 303, Tucson, AZ 85721-0036, USA					
	Tel: 520 626 9595					
	Fax: 520 621 1259					
	Email: http://genome.arizona.edu					
	PCR Primers					
	FORWARD: TAA TAC GAC TCA CTA TAG GG					
	BACKWARD: CAC TCA TTA GGC ACC CCA					
	Plate: 0026 row: D column: 24					
	Seq primer: CAC TCA TTA GGC ACC CCA					
	Class: BAC ends.					
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source	1. .376 /organism="Oryza australiensis"					
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	/db_xref="taxon:4532"					
	/clone="OA_ABA0026D24"					
	/tissue_type="young leaves"					
	/lab_host="DH10B TI phage resistant"					
	/clone_lib="OA_ABA"					
	/note="Vector: pGIBAC1; site_1: HindIII; site_2: HindII"					

ORIGIN

Query Match	21.4%	Score 307.2;	DB 9;	Length 376;		
Best Local Similarity	94.1%	Pred. No. 2e-66;				
Matches	354;	Conservative	0;	Mismatches 13;	Indels 9;	Gaps 3;

C	21	97	6.8	723	9	CL817465
C	22	94.4	6.6	491	9	CL739488
C	19	98.8	6.9	771	9	CL753477
C	20	98.4	6.9	754	9	CL858870
C	18	99	6.9	845	8	AQ912524
C	19	98	6.9	771	9	CL753477
C	20	98.4	6.9	754	9	CL858870
C	21	97	6.8	723	9	CL817465
C	22	94.4	6.6	491	9	CL739488
C	23	93.4	6.5	365	6	C72467
C	24	92.2	6.4	561	9	CL752715 OR_BBA011

FEATURES	FEATURES	ORIGIN
Source	source	Query Match Best Local Similarity 9.1%; Score 130.8; DB 9; Length 612; Matches 191; Conservative 0; Mismatches 57; Indels 6; Gaps 2;
		QY 510 AATGTGCCATGATCCTGCATCATGCCAAGATTATTCCTCACATTTCCTCC 569
		QY 376 AATGTGCCATGATCCTGCATCATGCCAAGATTATTCCTCACATTTCCTCC 317
		Db 570 TATCGCTCTAGTC-----GTCTGTTGGAGCTAAATTATGAAAAGCAGCTGCTG 622
		QY 316 TATCGCTCTAGTC-----GTCTGTTGGAGCTAAATTATGAAAAGCAGCTGCTG 257
		QY 623 AGGAAGCTAGCTGGTGGAGAAATTAGTTAGCTGAGAATTCTAATTCCGAGAACAGCTGCTG 682
		Db 256 AGGAAGCTAGCTGGTGGAGAAATTAGCTGAGAATTCTAATTCCGAGAACAGCTGCTG 198
		QY 683 ATTACAGATTCTATAATTAGTAAAGCTGGACTGTT-GGGAGCTCTGTCAGCC 138
		QY 197 ATTACAGATTCTAGAATTAGTAAAGCTGGACTGTT-GGGAGCTCTGTCAGCC 138
		QY 742 GGAGATTCTGTGAGAACGCTGCAGCTGCTAGTTGAGCTTGAC 801
		Db 137 GGAGATTCTGGAGAACGCTGCAACTGCTAGTTGAGCTTCCCACAGACCCCTAGTTGAC 78
		QY 802 TCTAGCTGATCGATTCACTCTATTATACACCTGCTCTAGCTTACACGTAG 861
		Db 77 TCCAGCTGATCGATTCACTCTATTATACACCTGCTCTAGCTTACACGTAG 18
		QY 862 CCAAGACTTGATT 877
		Db 17 CCAAGACTTGATT 2
		RESULT 2
CL835542/c	CL835542	CL835542
LOCUS		612 bp DNA linear GSS 09-AUG-2004
DEFINITION		OR_CBA0059F08.f OR_CBA Oryza rufipogon genomic clone OR_CBA0059F08
ACCESSION		5' genomic survey sequence.
VERSION		CL835542
KEYWORDS		CL835542.1 GI:51081152
SOURCE		GSS.
ORGANISM		Oryza rufipogon
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
		Ehrhartoideae; Oryzeae; Oryza.
REFERENCE		1 (bases 1 to 612)
AUTHORS		Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
TITLE		OMAP project
JOURNAL		Unpublished (2004)
COMMENT		Contact: Rod A. Wing
Arizona Genomics Institute		University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA		Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595		Fax: 520 621 1259
Fax: 520 621 1259		Email: http://genome.arizona.edu
Email: http://genome.arizona.edu		PCR Primers
PCR PRIMERS		FORWARD: TAA TAC GAC TCA CTA TAG GG
FORWARD: TAA TAC GAC TCA TTA GGC ACC CCA		BACKWARD: CAC TCA TTA GGC ACC CCA
BACKWARD: CAC TCA TTA GGC ACC CCA		Plate: 0059 row: F column: 08
Seq primer: TAA TAC GAC TCA CTA TAG GG		Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.		Class: BAC ends.
FEATURES	Location/Qualifiers	Location/Qualifiers
Source	1. .612 /organism="Oryza rufipogon" /mol_type="genomic DNA" /db_xref="taxon:4529" /clone="OR_CBA0081H21" /tissue_type="young leaves" /dev_stage="2 week old seedlings" /lab_host="DH10B T1 phage resistant" /clone_lib="OR_CBA" /note="vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII; drk treated 36 hrs before harvest"	1. .784 /organism="Oryza rufipogon" /mol_type="genomic DNA" /db_xref="taxon:4529" /clone="OR_CBA0081H21" /tissue_type="young leaves" /dev_stage="2 week old seedlings" /lab_host="DH10B T1 phage resistant" /clone_lib="OR_CBA" /note="vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII; drk treated 36 hrs before harvest"
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		QY 581 GTCGCTCTGGAGCTAAATTATGAAAAGCAGCTGCTGAGAAGCTAGCTGGAGA 640
		Db 433 GGCCTGTTGGGGAGATTAGATCCGAGAACGCTGCTGAGAAGCTAGCTGGAGA 374
		QY 641 ATCTAGAGAATTG----AGTTCTACGTTCATTCAGATCTACAGATCTACAGATCTC 696
		Db 373 ATCTAGAGAATTG----AGTTCTACGTTCATTCAGATCTACAGATCTC 314
		QY 697 ATAATTAGTAAAGCTGGACTGTT-GGGAGCTCTGAGATTCTAGTCAGATCTACAGATCTC 754
		Db 313 AGATCTGGTAAAGTGGACTGTTGGGGAGCTCTGCAACTGGAGATTCTAGGA 254
		QY 755 GAAGCTGCAGCTGCTAGAAGCTTCCCCAACAGACCCCTAGTTGACTCTAGCTGATCGA 814
		Db 253 GAAGCTGCAGCTGCTAGAAGCTCCACAGGCCTTAGGCTTCGTCAGTGAGC 194
		QY 815 TTCACTCTATT 828
		Db 193 TTTCAGCTATA 180

	Query Match	8.8%	Score 126; DB 9;	Length 784;		
Best Local Similarity	80.1%	Pred. No. 1.4e-20;				
Matches 173; Conservative	0;	Mismatches 40; Indels 3; Gaps 2;				
Qy	581 GTCGCTGTTGGAGCTAAATATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGTAGA	640				
Db	391 GACCTGTTGGAGCTAAATATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGTAGA	450				
Qy	641 ATCTGAAGAATTGACTTCAGTCATTCTCCAGATCTCAATTACAGATCTTATAA	700				
Db	453 AACCCAGC-TTCTGGCTCTAGTCATTCTAGATCTACAAGATCTTAGAA	510				
Qy	451 AACCCAGC-TTCTGGCTCTAGTCATTCTAGATCTACAAGATCTTAGAA	508				
Db	701 TTAGGTAAGAGCTGGACTGTTGGG-AGCTCTGTCAGCCGAGATTCTGTGAGA	759				
Qy	701 TTAGGTAAGAGCTGGACTGTTGGG-AGCTCTGTCAGCCGAGATTCTGTGAGA	759				
Db	509 TCTAGGTAAGATGCTGGACTGTTGGGAGCTCTGGCAACTGGAGATCTTAGGAGA	568				
Qy	760 TCGAGCTGCTAGAAGCTCCCCAACAGACCCCTAG 795					
Db	569 TGCAGTTGCTAGAACAGACCCCTAG 604					
RESULT 4						
CL855333	CL855333	829 bp	DNA	linear	GSS 16-AUG-2004	
DEFINITION	OR_CBa0085C07.f OR_CBa	Oryza rufipogon	genomic clone	OR_CBa0085C07		
ACCESSION	5', genomic survey	sequence.				
VERSION	CL855333					
KEYWORDS	CL855333.1	GI:51263573				
SOURCE	Oryza rufipogon					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Gramineae; Oryzeae; Oryza.					
REFERENCE	1 (bases 1 to 829)					
AUTHORS	Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.					
TITLE	OMAP project					
JOURNAL	Unpublished (2004)					
COMMENT	Contact: Rod A. Wing					
	Arizona Genomics Institute					
	University of Arizona					
	Forbes Building Room 303, Tucson, AZ 85721-0036, USA					
	Tel: 520 626 9595					
	Fax: 520 621 1259					
	Email: http://genome.arizona.edu					
PCR PRIMERS	FORWARD: TAA TAC GAC TCA CTA TAG GG					
BACKWARD: CAC TCA TTA GGC ACC CCA						
Plate: 0085 row: C column: 07						
Seq primer: TAA TAC GAC TCA CTA TAG GG						
Tel: 520 626 9595						
Fax: 520 621 1259						
Email: http://genome.arizona.edu						
PCR PRIMERS	FORWARD: TAA TAC GAC TCA CTA TAG GG					
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Plate: 0085 row: C column: 07						
Seq primer: TAA TAC GAC TCA CTA TAG GG						
Class: BAC ends.						
FEATURES	Location/Qualifiers					
FORWARD: TAA TAC GAC TCA CTA TAG GG	1. .829					
BACKWARD: CAC TCA TTA GGC ACC CCA	/organism="Oryza rufipogon"					
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FORWARD: TAA TAC GAC TCA CTA TAG GG	1. .829					
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BACKWARD: CAC TCA TTA GGC ACC CCA	/organism="Oryza rufipogon"					
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Class: BAC ends.	/clone="OR_CBa0085C07"					
FEATURES	Location/Qualifiers					
FORWARD: TAA TAC GAC TCA CTA TAG GG	1. .829					
BACKWARD: CAC TCA TTA GGC ACC CCA	/organism="Oryza rufipogon"					
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FORWARD: TAA TAC GAC TCA CTA TAG GG	1. .829					
BACKWARD: CAC TCA TTA GGC ACC CCA	/organism="Oryza rufipogon"					
Plate: 0085 row: C						

QY	768	CTAGAAGCTCCCAAACAGACCCCTAG	795	CL811645 AAAAGCTGGACTGTTGGAAAGCTCTAGCAAATGGCCCTAG	613
Db	614	CTAGAAGCTCCCAAATAGGCCCTAG	641	CL811645 OR_CBA0027D24.r OR_CBA Oryza rufipogon genomic clone OR_CBA0027D24	486 bp DNA linear GSS 09-AUG-2004
ACCESSION				3', genomic survey sequence.	
VERSION				CL811645	
KEYWORDS				GSS.	
SOURCE				Oryza rufipogon	
ORGANISM				Oryza rufipogon	
REFERENCE				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	
AUTHORS				Kim,H., Yu,Y., Stum,D., Yost,D., Stum,D., Rao,K., Luo,M., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.	
TITLE				1 (bases 1 to 486)	
JOURNAL				Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.	
COMMENT				OMAP project	
PCR PRIMERS				Unpublished (2004)	
FORWARD				Contact: Rod A. Wing	
BACKWARD				Arizona Genomics Institute	
Insert Length:				University of Arizona	
Plate: 0100				Forbes Building Room 303, Tucson, AZ 85721-0036, USA	
Row: G				Tel: 520 626 9595	
Column: 05				Fax: 520 621 1259	
Seq primer: TAA TAC GAC TCA CTA TAG GG				Email: http://genome.arizona.edu	
Class: BAC ends.				PCR PRIMERB	
Location/Qualifiers				FORWARD: TAA TAC GAC TCA CTA TAG GG	
FEATURES				BACKWARD: CAC TCA TTA GGC ACC CCA	
Source				Plate: 0027 row: D column: 24	
ORIGIN				Seq primer: CAC TCA TTA GGC ACC CCA	
Query Match				Class: BAC ends.	
Best Local Similarity				Location/Qualifiers	
Matches 174; Conservative 0; Mismatches 29; Indels 3; Gaps 3;				1. .486	
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QY	641	ATCTGAAGAATTGCA-----GTTCTACCGTCATTCCAGATCTCACAT	685	/db_xref="taxon:4529"	
Db	68	ATCTGGAGAACCCAGCTCTGGCTCTAGTCATTTCAGATCTCACAC	127	/clone="OR_CBA0027D24"	
QY	686	TACAGATCTATAATTAGTAAAGCTGGACTGTT--GGGAGCTCTGTCAGCCGG	743	/tissue_type="young leaves"	
Db	128	TACAGATCTCGAGAACGCTGGAAAAGCTGGACTGTTGGGGAGCTCTGACAACTGG	187	/dev_stage="2 week old seedlings"	
QY	744	AGATTCTGTGAGAACGCTGCACTGCTAGAACGCTTCCCCAACAGACCCCTAGTGTACTC	803	/lab_host="DH10B T1 phage resistant"	
Db	188	AGATTCAGTAGAACGCTACAGCTGCTAGAACGCTGGAGCTGAGCTGAGTGTG	613	/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII; drk treated 36 hrs before harvest"	
QY	554	AAAAGCTGGACTGTGGG-AGCTCTGTCAGCCGGAGATTCTGTGAGAACGCTGAGCTG	767		
Db	554	CTTCTGACTTCTA-GTTTCTAGATCTACAACATACAGATTCTAGAACGATCTAGGAA	553		
QY	709	AAAGCTGGACTGTGGG-AGCTCTGTCAGCCGGAGATTCTGTGAGAACGCTGAGCTG	767		
Db	768	CTAGAAGCTCCCAAACAGACCCCT	793		
QY	614	CTAGAAGCTCCCAAATAGGCCCT	639		
Db	248	ACTCTCCCTTGGGCTGCAGTAA	272		

RESULT 7

CL708436 CL708436 linear GSS 26-JUL-2004

DEFINITION OR_BBa0029A21.r OR_BBa *Oryza rufipogon* genomic clone OR_BBa0029A21
 ACCESSION 3', genomic survey sequence.
 CL708436
 VERSION CL708436.1 GI:50595474
 KEYWORDS GSS.
 SOURCE *Oryza rufipogon*
 ORGANISM *Oryza rufipogon*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 820)
 AUTHORS Kim,H., Yu,Y., Wissottski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
 Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
 Wing,R.
 TITLE Unpublished (2004)
 JOURNAL PCR Primers
 COMMENT PCR project
 Unpublished (2004)
 Contact: Rod A. Wing
Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: <http://genome.arizona.edu>

FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0029 row: A column: 21
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.

FEATURES Location/Qualifiers

source

1. .665
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BBa0029A21"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /clone_lib="OR_BBa"
 /note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII;
 drk treated 36 hrs before harvest"

ORIGIN

Query Match Best Local Similarity 7.5%; Score 107.8; DB 9; Length 665;
 Matches 173; Conservative 0; Mismatches 47; Indels 17; Gaps 2;

QY 580 AGTCGTCGTGGAGCTAAATTATGAAAAGCAGCTGCTGAGAACCTAGCTGGTGAG 639
 Db 334 AGCCCTGTTAGGGAGCTTGAAGATCTTAAGAAGCTGCTGAGAACCTACCTGGAG 393

QY 640 AATCTGAGAATTGAGT-----TCTACGTTCATTCAGATTCAA 684
 Db 394 AATCTGAAAACCTGAGAACCTAGCTCTGGCTCTAGTTACAGATTCAA 453

QY 415 AATCTGAGAATTGAGT-----TCTACGTTCATTCAGATTCAA 684
 Db 454 CTACATATTTCAGAATCTAAGTAATAGCTGGACTGTTCTGCCA 513

QY 685 TTACAGATTCTATAATTAGTAAAAGCTGGACTGTT-GGGAGCTCTGTCAAGCCG 742
 Db 743 GAGATCTGTGAGAACGCTGGACTGTTCTGCCA 799

Db 514 AAGATTCTAGGAGAGCTGCAGCTGTAGAACCTCCACCAACAGACCTTAACAGT 570

QY 743 GAGATCTGTGAGAACGCTGGACTGTTCTGCCA 799
 Db 535 AAGATTCTAGGAGAGCTGCAGCTGTAGAACCTCCACCAACAGACCTTAACAGT 591

RESULT 9

CL854157 LOCUS CL854157 820 bp DNA linear GSS 16-AUG-2004
 DEFINITION OR_CBA0083J07.f OR_CBA *Oryza rufipogon* genomic clone OR_CBA0083J07
 5', genomic survey sequence.

ACCESSION CL854157
 VERSION CL854157.1 GI:51260708
 KEYWORDS GSS.

REFERENCE 1 (bases 1 to 824)
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
 TITLE OMAP Project

DEFINITION OR_BBa0098L11.r OR_BBa *Oryza rufipogon* genomic clone OR_BBa0098L11
 ACCESSION 5', genomic survey sequence.
 CL782578
 VERSION CL782578.1 GI:50862174
 KEYWORDS GSS.

SOURCE *Oryza rufipogon*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 824)
 AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
 Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
 TITLE OMAP Project

JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: <http://genome.arizona.edu>

PCR PRIMERS
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0083 row: P column: 11
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES
 SOURCE Location/Qualifiers
 1. . 824 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BBa009BL11"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /cloneLib="OR_BBa"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 7.5%; Score 107.8; DB 9; Length 824;
 Best Local Similarity 73.0%; Pred. No. 5.4e-16;
 Matches 173; Conservative 0; Mismatches 47; Indels 17; Gaps 2;

Qy 589 TTGGGAGCTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAAG 648
 Db 517 TGGGGAGCTAAATTCTAAGAACAGCTGCTGAGAACATGAAA 458

Qy 649 ATTGTGAGTTCTAC-----GTTCATTCAGATTACAATTACAGATT 693
 Db 457 AAGCTGGAAACTCAACTCTGGGTTCTAGTTCAATTCCAGATTACAATTAGATT 398

Qy 694 CTATAATTAGTAAAGCTGGACTGTT-GGGAGCTCTGTAGCCGGAGATTCTG 751
 Db 397 CTCAGAATCTGGATAAAAGCTGGACAGTTGGCGAGCTCTAGCACTCGAGATTCTA 338

Qy 752 TGAGAAGCTGCAAGCTGCTAGAACAGACCCCTAGTTGACTCTAGCT 808
 Db 337 GGAGAAGCTGCAAGCTACTAGAACGCTCTCCAAATAAGCTTAGTGGCAGCT 281

RESULT 11

CL746481/C CL746481 784 bp DNA linear GSS 27-JUL-2004
 LOCUS OR_BBa0083P11.f OR_BBa Oryza rufipogon genomic clone OR_BBa0083P11
 DEFINITION 5' genomic survey sequence.

ACCESSION CL746481
 VERSION GI:50688740
 KEYWORDS GSS.
 SOURCE
 ORGANISM Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 784)
 AUTHORS Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
 Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
 Wing,R.

TITLE OMAP Project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: <http://genome.arizona.edu>

PCR PRIMERS
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0021 row: N column: 19
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.

FEATURES
 SOURCE Location/Qualifiers
 1. . 784 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_BBa0083P11"
 /tissue_type="young leaves"
 /lab_host="DH10B-T1 phage resistant"
 /cloneLib="OR_BBa"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 7.3%; Score 105.2; DB 9; Length 784;
 Best Local Similarity 77.9%; Pred. No. 2.4e-15;
 Matches 159; Conservative 0; Mismatches 28; Indels 17; Gaps 2;

Qy 585 TCTGTTGGAGCTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAAGATCT 644
 Db 204 TGTAGGGAGCTTAAGATTCAGATTCTCAGATTACA 145

Qy 645 GAAGAATTGA-----GTTCTACGGTCATTCTCCAGATTACAATTACA 689
 Db 144 GAAGAAGCTGAAAAACCACTCTGGCTCTAGTTCAATTCCAGATTCTA 85

Qy 690 GATCTTATAATTAGTAAAGCTGGACTGTT-GGGAGCTCTGTAGCCGGAGAT 747
 Db 84 GATTCTTGAATCTGGATAAAAGCTGGACTGTTAAAGAACGCTCTGTCAACTGGAGAT 25

Qy 748 TCTGTGAGAAGCTGGAGCTGCTAG 771
 Db 24 TCTAGGAGAAGCTGGAGCTGCTAG 1

RESULT 12

CL807668 CL807668 707 bp DNA linear GSS 09-AUG-2004
 LOCUS OR_CBA0021N19.r OR_CBA Oryza rufipogon genomic clone OR_CBA0021N19
 DEFINITION 3' genomic survey sequence.

ACCESSION CL807668
 VERSION GI:51045250
 KEYWORDS GSS.
 SOURCE
 ORGANISM Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 707)
 AUTHORS Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
 Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
 Wing,R.

TITLE OMAP project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: <http://genome.arizona.edu>

PCR PRIMERS
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert Length: 161 Std Error: 0.00
 Plate: 0021 row: N column: 19
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.

FEATURES
 SOURCE Location/Qualifiers

source 1. .707
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_CBA0021N19"
 /tissue_type="young leaves"
 /dev_stage="2 week old seedlings"
 /lab_host="DH10B T1 phage resistant"
 /clone_lib="OR_CBA"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
 drk treated 36 hrs before harvest"

ORIGIN

	Query Match	Score	DB	Length
Best Local Similarity	7.3%	104.6	9	707
Matches	169;	Conservative	0;	Mismatches 49; Indels 15; Gaps 2;

QY 579 TAGTCGCTCTGGAGCTAAATTATGAAAAGCAGCTGTGAGAAGCTAGCTGGTGA 638
 Db 296 TAGGCCTGTTAGGGAACTTAATTCTGAGAACAGCTGCTAAGAGCTAGCTGGTGA 355

QY 639 GAATCTGAGAAATTGAA-----GTTCTACGTTCATCTCCAGATCTACAA 684
 Db 356 GAATTGGAGAACGCTGTAACCCAGCTCTGCTTAGCTGATTTCAAGTCTACAA 415

QY 685 TTACAGATTCTATAATTAGTAAGCTGACTGTTG-GGAGCTCTGTCCAGCCGG 743
 Db 416 TTACATATTCTCAGAATCTAGATAAAAGCTAGACTGTTGAGGAGCTTTAACAAATAA 475

QY 744 AGATCTGTGAGAACGCTGCTAGAAGCTTCCCCAACAGACCCCTAGT 796
 Db 476 AAATTCTAAAGAACCTGCAAGCTCTCCAAACATACCCGGTGGT 528

RESULT 13

	LOCUS	DEFINITION	VERSION	KEYWORDS	ACCESSION	VERSION	KEYWORDS	ACCESSION	VERSION	KEYWORDS	ACCESSION	VERSION	KEYWORDS	
CL843536	CL843536	757 bp DNA linear GSS 09-AUG-2004	AQ328957	nbxbo044119f	OR_CBA0072P12.r OR_CBA	09-AUG-2004	nbxb0044119f	CUGI Rice BAC Library	590 bp DNA linear GSS 08-JAN-1999	AQ328957	nbxb0044119f	CUGI Rice BAC Library	08-JAN-1999	
DEFINITION	OR_CBA0072P12.r OR_CBA	Oryza rufipogon genomic clone OR_CBA0072P12	DEFINITION	Oryza sativa (japonica cultivar-group)	OR_CBA0072P12	DEFINITION	Oryza sativa (japonica cultivar-group)	OR_CBA0072P12	nbxb0044119f	cultivar-group	nbxb0044119f	cultivar-group	nbxb0044119f	
ACCESSION	CL843536	3' genomic survey sequence.	ACCESSION	Oryza sativa (japonica cultivar-group)	CL843536	3' genomic survey sequence.	ACCESSION	Oryza sativa (japonica cultivar-group)	CL843536	3' genomic survey sequence.	ACCESSION	Oryza sativa (japonica cultivar-group)	CL843536	
VERSION	CL843536.1	GI:51089146	VERSION	Oryza sativa (japonica cultivar-group)	CL843536.1	GI:51089146	VERSION	Oryza sativa (japonica cultivar-group)	CL843536.1	GI:51089146	VERSION	Oryza sativa (japonica cultivar-group)	CL843536.1	
KEYWORDS	GSS.		KEYWORDS	Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza rufipogon		KEYWORDS	Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza rufipogon		KEYWORDS	Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza rufipogon		KEYWORDS	Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza rufipogon	
SOURCE			SOURCE			SOURCE			SOURCE		SOURCE		SOURCE	
ORGANISM			ORGANISM			ORGANISM			ORGANISM		ORGANISM		ORGANISM	

REFERENCE 1 (bases 1 to 757)
 AUTHORS Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
 TITLE OMAP project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0072 row: P column: 12
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends
 FEATURES source
 SOURCE 1. .757
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="nbxb0044119f"
 /tissue_type="Leaf"
 /lab_host="E. coli DH10B"
 /clone_lib="CUGI Rice BAC Library"
 /note="Vector: pBelBAC1; Site_1: HindIII; site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp

FEATURES source
 SOURCE 1. .757
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_CBA0072P12"
 /tissue_type="young leaves"

(Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of *Arabidopsis*, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.

ORIGIN

Query Match 7.2%; Score 104; DB 8; Length 590;
Matches 161; Conservatve 0; Mismatches 31; Indels 19; Gaps 2;
Qy 592 GGGAGCTTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAGAATCTGGAGAAT 651
Db 553 GGGAGTTAACGATTCTAAGAACGAGCTGCTGAGAAGCTAGCTGGTGAGAATCTGGATAA----- 500
Qy 652 TTGAGTTCTACGTTCATCTCCAGATTCTACATTACAGATTCTATAATTAGTAAA 711
Db 499 -----GTTCATTTCTCTGATTCTACACTACAGATTCTACAAATCTGGATAAA 451
Qy 712 AGCTGGACTCTTT--GGAGCTTCTGTCAGCCGGAGATTCTGTGAGAAGCTGCAGCTGCT 769
Db 450 ATCTGGACTCTTGGGGAGCTTCTGGCAACTTGAGATTAGGAGAAGCTGCAGCTANT 391
Qy 770 AGAACGCTCCCCAACAGACCCCTAGTTGTA 800
Db 390 AAAAGCTCCCCAACAGGCCCTGATTAGGA 360

RESULT 15

/clone lib="TAMU Rice Japonica Nipponbare BAC library
(Hind III)"
/notee="Vector: V41"
ORIGIN
Query Match 7.0%; Score 100.6; DB 9; Length 431;
Matches 159; Conservatve 0; Mismatches 34; Indels 8; Gaps 3;
Qy 598 TAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAGAATCTGAGAATTGAGT 657
Db 1 TAAATTCTGAGAAGCAGCTGCTGAGAATCTGAGAATTCTGAGACCTAGCT 59
Qy 658 TCTACG-----TCATTCAGATTCTACAATTACAGATTCTATAATTAGTAAA 712
Db 60 TTGACTCTAACTCATTTCTAGATTCTACACTACAGATTCTAAATCTGGATAAA 119
Qy 713 GCTGACTGTGTTG--GGAGCTTCTGTCAGCCGGAGATTCTGTGAGAAGCTGCAGCTGCTA 770
Db 120 GCTGAACTGTGTTGGAGGAGCTTCTGACAACTGAGATTCTAAAGAGAAGCTGCAGCTGTTA 179
Qy 771 GAAGCTCCCCAACAGACCC 791
Db 180 GAAACACCTCTAACAGGCC 200
Search completed: September 23, 2005, 19:20:35
Job time : 3430 secs

CG206879 CG206879 LOCUS CG206879 DEFINITION TOS0501 TAMU Rice Japonica Nipponbare BAC Library (Hind III) *Oryza sativa* (*japonica* cultivar-group) genomic clone TOSJNBh024F14h, genomic survey sequence.
ACCESSION CG206879
VERSION CG206879.1
KEYWORDS GSS.
SOURCE GSS.
ORGANISM *Oryza sativa* (*japonica* cultivar-group)
Oryza sativa (*japonica* cultivar-group)
Ehrhartoideae; *Oryzeae*; *Oryza*.
REFERENCE 1
AUTHORS Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.
TITLE BAC end sequences to close the gaps of a rice physical map at TAMU
JOURNAL Unpublished (2003)
COMMENT Contact: Wu C
Department of Soil and Crop Sciences and Institute for Plant
Genomics and Biotechnology
Texas A & M University
TAMU 2474, College Station, TX 77843-2474, USA
Tel: 979 862 4800
Fax: 979 862 4790
Email: c-wu@neo.tamu.edu
Seq primer: M13 Universal Reverse AACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 431.
Location/Qualifiers

FEATURES

source
1. .431
/organism="Oryza sativa" (*japonica* cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="TOSJNBh024F14h"
/tissue_type="leaf"
/lab_host="E. coli DH10B"

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: September 23, 2005, 17:01:48 ; Search time 714 Seconds
(without alignments)
13447.233 Million cell updates/sec

Title: US-10-602-166-2
Perfect score: 1436
Sequence: 1 cattcagaatcatctccagc.....tatcaagggttcaacctgg 1436

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

ALIGNMENTS

RESULT 1
US-09-848-696-2
; Sequence 2, Application US/09848696
; Patent No. US20010051713A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTER-SPECIFIC GENE AND TRANSGENIC PLANT TR-
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/09/848, 696
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 2
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-848-696-2

Query Match 100.0%; Score 1436; DB 9; Length 1436;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length	DB ID	Description
1	1436	100.0	1436	9	US-09-848-696-2 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli
2	1436	100.0	1436	18	US-10-602-166-2 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli
3	1436	100.0	3003	9	US-09-848-696-1 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli
4	1436	100.0	3003	18	US-10-602-166-1 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli
5	1196	83.3	1196	9	US-09-848-696-3 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli
6	1196	83.3	1196	18	US-10-602-166-3 Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli
7	240	9	107.4	7.5	US-10-602-166-10 Sequence 10, Appli Sequence 87679, A Sequence 7, Appli Sequence 7, Appli Sequence 30221, A Sequence 72585, A Sequence 2616, Ap Sequence 4, Appli Sequence 34782, A Sequence 44842, A Sequence 89687, A Sequence 44845, A Sequence 1892, Ap Sequence 7, Appli Sequence 4, Appli Sequence 6, Appli Sequence 5, Appli Sequence 90519, A Sequence 1, Appli Sequence 1653, Ap Sequence 80401, A Sequence 97252, A Sequence 45803, A Sequence 44654, A Sequence 28, Appli Sequence 316, App Sequence 1347, Ap Sequence 386, App Sequence 125688, A Sequence 6577, Ap Sequence 276, App Sequence 255, App Sequence 1025, Ap Sequence 641, App Sequence 27, Appli Sequence 240, App Sequence 2, Appli Sequence 132592,

Db	1.081	TATGCTTAATCTCTTACTGGACTTAGTTGGACAATCGTAATGCATTCTCGTGCCA	1140
Qy	1.141	TCTCTATAATACGGCCTGCTAGCTTGCCTCTGTATCTGCACACAACTAGCTGGCAA	1200
Db	1.141	TCTCTATAATACGGCCTGCTAGCTTGCCTCTGTATCTGCACACAACTAGCTGGCAA	1200
Qy	1.201	AGTCCTCAAGGCCAACCGCCTCCATCTCTCCAGCTCCTCCATGGGTCCTCGT	1260
Db	1.201	AGTcCTCAAGGCCAACCGCCTCCATCTCTCCAGCTCCTCCATGGGTCCTCGT	1260
Qy	1.261	CGCCATGCCATGCCATGGCTCTCATGGTGCAGAGATATCCAGCATGCTGAATTAACT	1320
Db	1.261	CGCCATGCCATGCCATGGCTCTCATGGTGCAGAGATATCCAGCATGCTGAATTAACT	1320
Qy	1.321	TGACGCATATCATCTCATCACTTGCAATTCACTTCTGGATTGTGCAGACATGTTA	1380
Db	1.321	TGACGCATATCATCTCATCACTTGCAATTCACTTCTGGATTGTGCAGACATGTTA	1380
Qy	1.381	GCTGATCAGTAAACGTTGCCGTTGAATTGGTCTTATCAGGTGGTCAACCTGG	1436
Db	1.381	GCTGATCAGTAAACGTTGCCGTTGAATTGGTCTTATCAGGTGGTCAACCTGG	1436

RESULT 2
US-10-602-166-2

Db	241	AATTGTTTATTTTGCTACAATCGACTAGTAGCAGTAGCAGAGCTAGCGTAAAGTCG 300	Db	1321	TGACGCATATCATCTCATCATCACTTCGATTCACTCTGATTTGAGACATGTTA 1380
Qy	301	TGTTCCGATCACCTGAGAACCGTCAGGTGGTTGTCAGCCGTCAGCCGATCAGAAT 360	Qy	1381	GCTGATCAGTAACGTGCGTGTGAATTGGCTTATCAGGGTTCAACCTGG 1436
Db	301	TGTTCCGATCACCTGAGAACCGTCAGGTGGTTGTCAGCCGTCAGCCGATCAGAAT 360	Db	1381	GCTGATCAGTAACGTGCGTGTGAATTGGCTTATCAGGGTTCAACCTGG 1436
Qy	361	TCGGAGATCCGCCGTCGGTTCTTCTGAAATCTGCAAGTCCCAGCAGCAGCAG 420	RESULT 3	US-09-848-696-1	
Db	361	TCGGAGATCCGCCGTCGGTTCTTCTGAAATCTGCAAGTCCCAGCAGCAGCAG 420	; Sequence 1, Application US/09848696		
Qy	421	ACCAAGAGCAAAGGGTTGATACTTGACTGCACTAGTAGCTAGCTAGAGGG 480	; Patent No. US20010051713A1		
Db	421	ACCAAGAGCAAAGGGTTGATACTTGACTGCACTAGTAGCTAGCTAGAGGG 480	; GENERAL INFORMATION:		
Qy	481	TCGTTCCATGTCGCTCACGCCGTCAGGGAGTTGATACTTGACTGCACTAGAGGG 540	; APPLICANT: AN, GYN HEUNG		
Db	481	TCGTTCCATGTCGCTCACGCCGTCAGGGAGTTGATACTTGACTGCACTAGAGGG 540	; APPLICANT: JEON, JONG-SEONG		
Qy	541	AGGATATATCTCACATTCTCTATCGCTCTAGTCGCTGATGCCATCATCGCC 600	; APPLICANT: CHUNG, YONG-YOON		
Db	541	AGGATATATCTCACATTCTCTATCGCTCTAGTCGCTGATGCCATCATCGCC 600	; PRIORITY: LEE, SI CHUL		
Qy	601	AAATTATGAAAGCAGCTGCTGAGAGCTAGTCGGTGGAGAATCTGAGAAATTGAGTCT 660	; TITLE OF INVENTION: DNA COMPRISING RICE ANTHE-R-SPECIFIC GENE AND TRANSGENIC PLANT TR-		
Db	601	AAATTATGAAAGCAGCTGCTGAGAAATCTGAGAAATTGAGTCT 660	; TITLE OF INVENTION: THEREWITH		
Qy	661	ACGTTCATTCTCCAGATCTACAAATTACAGATTCTTATAATTAGGAAAAGCTGGACT 720	; FILE REFERENCE: S-30723A		
Db	661	ACGTTCATTCTCCAGATCTACAAATTACAGATTCTTATAATTAGGAAAAGCTGGACT 720	; CURRENT APPLICATION NUMBER: US/09/848, 696		
Qy	721	GTGTTGGGAGCTCTGTCAGCCGGAGATTCTGTGAGAAGCTGAGCTGAGCTCCC 780	; CURRENT APPLICATION NUMBER: KR 98-50126		
Db	721	GTGTTGGGAGCTCTGTCAGCCGGAGATTCTGTGAGAAGCTGAGCTGAGCTCCC 780	; CURRENT FILING DATE: 2001-05-03		
Qy	781	CAACACAGACCCCTAGTGTACTCTAGCTGATCGATTCACTTATATACCTTGC 840	; PRIORITY FILING DATE: 1998-11-19		
Db	781	CAACACAGACCCCTAGTGTACTCTAGCTGATCGATTCACTTATATACCTTGC 840	; NUMBER OF SEQ ID NOS: 10		
Qy	841	TCTCTAGCTTATCAAAQGTAGCCAAAGCTTGAATTAAAGCTTAAATTGATTGT 900	; SOFTWARE: PatentIn Ver. 2.2		
Db	841	TCTCTAGCTTATCAAAQGTAGCCAAAGCTTGAATTAAAGCTTAAATTGATTGT 900	; SEQ ID NO 1		
Qy	901	TCTTTCATCGTAATTCACTTACCGACCTAGTCGGATTGAAATTTTAAATT 960	; LENGTH: 3003		
Db	901	TCTTTCATCGTAATTCACTTACCGACCTAGTCGGATTGAAATTTTAAATT 960	; TYPE: DNA		
Qy	961	TTAGAGCTGATTGATTTTCAGGGATTATTTCACGTATGAAATT 1020	; ORGANISM: Oryza sativa		
Db	961	TTAGAGCTGATTGATTTTCAGGGATTATTTCACGTATGAAATT 1020	; US-09-848-696-1		
Qy	1021	CCTATAATTATTATTTCAGGGATTATTTCACGTATGAAATT 1080	Query Match		
Db	1021	CCTATAATTATTATTTCAGGGATTATTTCACGTATGAAATT 1080	Best Local Similarity 100.0%; Pred. No. 0;		
Qy	1081	TATGCTTAATCTCTTACTGGACTTAGTGGACAAATTGTAATCTGG 1080	Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1081	TATGCTTAATCTCTTACTGGACTTAGTGGACAAATTGTAATCTGG 1080	Qy	1	CATTCAGAAATCATCTCCAGCTTACAATATAACCTCCATAATAGGTCTCTATGA 60
Qy	1141	TCTCTATAATACGGCCTCTAGCTGTTATCTGACACACAAGAACTAGCTGGCA 1200	Db	1	CATTCAGAAATCATCTCCAGCTTACAATATAACCTCCATAATAGGTCTCTATGA 60
Db	1141	TCTCTATAATACGGCCTCTAGCTGTTATCTGACACACAAGAACTAGCTGGCA 1200	Qy	61	TTCAAAATTGTCCTACAAATATAACCTCCAGCATGAAATTCCATACATAATTTCAG 120
Qy	1201	AGTCCTCAAGGGAAACCGCCCTCCATCTCCCTCCAGCTCCTCCATGGGTCCCTCGT 1260	Db	61	TTCAAAATTGTCCTACAAATATAACCTCCAGCATGAAATTCCATACATAATTTCAG 120
Db	1201	AGTCCTCAAGGGAAACCGCCCTCCATCTCCCTCCAGCTCCTCCATGGGTCCCTCGT 1260	Qy	121	CTAAATCAGATGCTGGGGAAAATCTAAGCGATTCAATATGCAAATTGATCACTGA 180
Qy	1261	CGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCC 1320	Db	121	CTAAATCAGATGCTGGGGAAAATCTAAGCGATTCAATATGCAAATTGATCACTGA 180
Db	1261	CGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCC 1320	Qy	181	AGTAACCTGAAAGAGAAATATCTCGTTAACATTAGTCGCTAGTATTAAACAACTAA 240
Qy	1081	TATGCTTAATCTCTTACTGGACTTAGTGGACAAATTGTAATCTGG 1080	Db	181	AGTAACCTGAAAGAGAAATATCTCGTTAACATTAGTCGCTAGTATTAAACAACTAA 240
Db	1081	TATGCTTAATCTCTTACTGGACTTAGTGGACAAATTGTAATCTGG 1080	Qy	241	AAATGTTTATTTAGTACAATCGAGTAGCTAGCTAGAGCTAGCGTAAGATCG 300
Qy	1141	TCTCTATAATACGGCCTCTAGCTGTTATCTGACACACAAGAACTAGCTGGCA 1200	Db	241	AAATGTTTATTTAGTACAATCGAGTAGCTAGCTAGAGCTAGCGTAAGATCG 300
Db	1141	TCTCTATAATACGGCCTCTAGCTGTTATCTGACACACAAGAACTAGCTGGCA 1200	Qy	301	TGTTCCGATCACCTGAGAACCGTCAGGTGGTTGTCAGCCGTCAGCCGATCAGAAT 360
Qy	1201	AGTCCTCAAGGGAAACCGCCCTCCATCTCCCTCCAGCTCCTCCATGGGTCCCTCGT 1260	Db	301	TGTTCCGATCACCTGAGAACCGTCAGGTGGTTGTCAGCCGTCAGCCGATCAGAAT 360
Db	1201	AGTCCTCAAGGGAAACCGCCCTCCATCTCCCTCCAGCTCCTCCATGGGTCCCTCGT 1260	Qy	361	TCGGAGATCCGCCGTCGGTTCTTCTGAAATCTGCAAGTCCCAGCAGCAGCAGCAG 420
Qy	1321	TGACGCATATCATCTCATCATCACTTCGATTCAACTTCTGGATTGTCAGACATGTTA 1380	Db	361	TCGGAGATCCGCCGTCGGTTCTTCTGAAATCTGCAAGTCCCAGCAGCAGCAGCAG 420
Qy	1321	TGACGCATATCATCTCATCATCACTTCGATTCAACTTCTGGATTGTCAGACATGTTA 1380	Qy	421	AGCAAGAGCAATGGCGTCACTGAGATATCCAGCATGCTGAATTAACT 1320
Db	1321	TGACGCATATCATCTCATCATCACTTCGATTCAACTTCTGGATTGTCAGACATGTTA 1380	Db	421	AGCAAGAGCAATGGCGTCACTGAGATATCCAGCATGCTGAATTAACT 1320
Qy	1321	TGACGCATATCATCTCATCATCACTTCGATTCAACTTCTGGATTGTCAGACATGTTA 1380	Db	481	TTCGTTCCATGTCGCTCTACGCCGTCGAATGTCGCAATGTCGATCATCGCC 540
Qy	1321	TGACGCATATCATCTCATCATCACTTCGATTCAACTTCTGGATTGTCAGACATGTTA 1380	Db	481	TTCGTTCCATGTCGCTCTACGCCGTCGAATGTCGCAATGTCGATCATCGCC 540

QY 541 AAGATTATTCCTCACATTTCCTCATCGCTCCTAGTCGTCGTTGGAGCTTA 600 ; CURRENT APPLICATION NUMBER: US/10/602,166
Db 541 AGGATTATTCCTCACATTTCCTCATCGCTCCTAGTCGTCGTTGGAGCTTA 600 ; CURRENT FILING DATE: 2003-06-24
QY 601 AATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAGAATTGAGTCT 660 ; PRIORITY NUMBER: US/09/848,696
Db 601 AATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAGAATTGAGTCT 660 ; PRIORITY FILING DATE: 2001-05-03
QY 661 AGTTCAATTCCAGATCTACAATTACAGATCTATAATTAGTAAAAGCTGGACT 720 ; PRIORITY APPLICATION NUMBER: KR 98-50126
Db 661 AGTTCAATTCCAGATCTACAATTACAGATCTATAATTAGTAAAAGCTGGACT 720 ; PRIORITY FILING DATE: 1998-11-19
QY 721 GTTGGGAGCTCTGTCAAGCCGGAGATCTGTGAGAAGCTGCAGCTGAGAATTGAGTCT 780 ; NUMBER OF SEQ ID NOS: 10
Db 721 GTTGGGAGCTCTGTCAAGCCGGAGATCTGTGAGAAGCTGCAGCTGAGAATTGAGTCT 780 ; SOFTWARE: PatentIn Ver. 2.2
QY 781 CAAACAGACCCCTAGTTGACTCTAGCTGATCGATTCACTTATACACCTTGC 840 ; SEQ ID NO: 1
Db 781 CAAACAGACCCCTAGTTGACTCTAGCTGATCGATTCACTTATACACCTTGC 840 ; LENGTH: 3003
QY 841 TCTCTAGTTATCAAACGTTAGCCAAGCTGTAATTGATTGATGT 900 ; TYPE: DNA
Db 841 TCTCTAGTTATCAAACGTTAGCCAAGCTGTAATTGATTGATGT 900 ; ORGANISM: Oryza sativa
QY 901 TCTTTCATGCTTAATTCACTTACCTACGCCAGCTTAGTCGGCATTTAAGCTTAATTGATTGATGT 960 ; US-10-602-166-1
Db 901 TCTTTCATGCTTAATTCACTTACCTACGCCAGCTTAGTCGGCATTTAAGCTTAATTGATTGATGT 960 ;
QY 961 TTAGAGCTGATTGATTTTCAGGGATTATTTCACGTTAGTCGGCATTTAAGCTTAATTGATTGATGT 1020 ;
Db 961 TTAGAGCTGATTGATTTTCAGGGATTATTTCACGTTAGTCGGCATTTAAGCTTAATTGATTGATGT 1020 ;
QY 1021 CCTATAAATTATAATTTCAGGGATTATTTCACGTTAGTCGGCATTTAAGCTTAATTGATTGATGT 1080 ;
Db 1021 CCTATAAATTATAATTTCAGGGATTATTTCACGTTAGTCGGCATTTAAGCTTAATTGATTGATGT 1080 ;
QY 1081 TATGCTTAATTATAATTTCAGGGATTATTTCACGTTAGTCGGCATTTAAGCTTAATTGATTGATGT 1140 ;
Db 1081 TATGCTTAATTATAATTTCAGGGATTATTTCACGTTAGTCGGCATTTAAGCTTAATTGATTGATGT 1140 ;
QY 1141 TCTCTATAATTACGGCTGCTAGCTTGCTCTGTATCTGACACAACTGCAATTCTGGCAA 1200 ;
Db 1141 TCTCTATAATTACGGCTGCTAGCTTGCTCTGTATCTGACACAACTGCAATTCTGGCAA 1200 ;
QY 1201 AGTCTCTAATTACGGCTGCTAGCTTGCTCTGTATCTGACACAACTGCAATTCTGGCAA 1260 ;
Db 1201 AGTCTCTAATTACGGCTGCTAGCTTGCTCTGTATCTGACACAACTGCAATTCTGGCAA 1260 ;
QY 1261 CGCCATGCCATGCCATGGCTCTCATGGGAGATACTGGCATGCTGAATTAACT 1320 ;
Db 1261 CGCCATGCCATGCCATGGCTCTCATGGGAGATACTGGCATGCTGAATTAACT 1320 ;
QY 1321 TGACGCATATCATCATCACTTCAGGAGATACTGGCATGCTGAATTAACT 1380 ;
Db 1321 TGACGCATATCATCATCACTTCAGGAGATACTGGCATGCTGAATTAACT 1380 ;
QY 1381 GCTGATCAGTAACGTTGCCGTGTGAATTGGCTTATCAGGTGGTCAACCTGG 1436 ;
Db 1381 GCTGATCAGTAACGTTGCCGTGTGAATTGGCTTATCAGGTGGTCAACCTGG 1436 ;

RESULT 4

US-10-602-166-1

; Sequence 1, Application US/10602166

; Publication No. US20040060084A1

; GENERAL INFORMATION:

; APPLICANT: AN, GYN HEUNG

; APPLICANT: JEON, JONG-SEONG

; APPLICANT: CHUNG, YONG-YOON

; APPLICANT: LEE, SI CHUL

; TITLE OF INVENTION: DNA COMPRISING RICE ANTER-SPECIFIC GENE AND TRANSGENIC PLANT TRA

; TITLE OF INVENTION: THEREWITH

; FILE REFERENCE: S-30723A

QY 601 AAATTATGAAAGCAGCTGAGAAGCTAGCTGGAGAATTGAGTCT 660 ; CURRENT APPLICATION NUMBER: US/10/602,166
Db 601 AAATTATGAAAGCAGCTGAGAAGCTAGCTGGAGAATTGAGTCT 660 ; CURRENT FILING DATE: 2003-06-24
QY 661 ACGTTCATTCTCAGATTCTACAATTACAGATTCTTATTCAGGAGCTAGCTGGTGAGTCT 720 ; PRIORITY NUMBER: US/09/848,696
Db 661 ACGTTCATTCTCAGATTCTACAATTACAGATTCTTATTCAGGAGCTAGCTGGTGAGTCT 720 ; PRIORITY FILING DATE: 2001-05-03
QY 721 GTTGGGAGCTCTGTCAAGCCGGAGATCTGTGAGAAGCTGCAGCTGCTAGAAGCTCCC 780 ; PRIORITY APPLICATION NUMBER: KR 98-50126
Db 721 GTTGGGAGCTCTGTCAAGCCGGAGATCTGTGAGAAGCTGCAGCTGCTAGAAGCTCCC 780 ; PRIORITY FILING DATE: 1998-11-19
QY 781 CAAACAGACCCCTAGTTGACTCTAGCTGATCGATTCACTTATACACCTTGC 840 ; NUMBER OF SEQ ID NOS: 10

Db 781 CAAACAGACCCCTAGTGTACTCTAGTGATTACCTTATACCTTCG 840
 Qy 841 TCTCTAGCTTATCAACGTTAGCCAGACTTGAAATTAAAGCTTAATGATTGATGT 900
 Db 841 TCTCTAGCTTATCAACGTTAGCCAGACTTGAAATTAAAGCTTAATGATTGATGT 900
 Qy 901 TCTTTCATCGTAATTCACTTACCGACCTTAGCGGATTTGAATTAAAGCTTAATGATTGATGT 900
 Db 901 TCTTTCATCGTAATTCACTTACCGACCTTAGCGGATTTGAATTAAAGCTTAATGATTGATGT 900
 Qy 961 TTAGAGCTGATTGATTTCAAGGGAAATTTCAGGGATTATTTCAGGTAAAGTTTA 960
 Db 961 TTAGAGCTGATTGATTTCAAGGGAAATTTCAGGGATTATTTCAGGTAAAGTTTA 960
 Qy 1021 CCTTATAAATTATAATTTCAGGGATTATTTCAGGTAAAGTTTA 1020
 Db 1021 CCTTATAAATTATAATTTCAGGGATTATTTCAGGTAAAGTTTA 1020
 Qy 1081 TATGCTTAATCTCTTACTTGGACTTAGTGGACAATTCGAATGCATCTCGCA 1140
 Db 1081 TATGCTTAATCTCTTACTTGGACTTAGTGGACAATTCGAATGCATCTCGCA 1140
 Qy 1141 TCTCTATAAACCGGCTTGCTAGCTTGCTCTGTATCTGACACAGAACCTGGCAA 1200
 Db 1141 TCTCTATAAACCGGCTTGCTAGCTTGCTCTGTATCTGACACAGAACCTGGCAA 1200
 Qy 1201 AGTCCTCAAGGGAAACGCCCTCCAATCTCTCCCTCCAGCTCCTGGGTCCCTCGT 1260
 Db 1201 AGTCCTCAAGGGAAACGCCCTCCAATCTCTCCCTCCAGCTCCTGGGTCCCTCGT 1260
 Qy 1261 CGCCATCGCCATCGCCATGGCTCTCATGGTGAGAGATATCCAGCATGCTGAATTAACT 1320
 Db 1261 CGCCATCGCCATCGCCATGGCTCTCATGGTGAGAGATATCCAGCATGCTGAATTAACT 1320
 Qy 1321 TGACCGATATCATCTCATCATCACTTGCAATTCAACTTGGATTGTCAGACATGTTA 1380
 Db 1321 TGACCGATATCATCTCATCATCACTTGCAATTCAACTTGGATTGTCAGACATGTTA 1380
 Qy 1381 GCTGATCAGTAAACGTTGCCGTGTTGAATTGGTCTTATCAGTTGGTCAACCTGG 1436
 Db 1381 GCTGATCAGTAAACGTTGCCGTGTTGAATTGGTCTTATCAGTTGGTCAACCTGG 1436
 RESULT 5
 US-09-848-696-3
 ; Sequence 3, Application US/09848696
 ; Patent No. US20010051713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AN, GYN HEUNG
 ; APPLICANT: CHUNG, YONG-YOON
 ; APPLICANT: LEE, SI CHUL
 ; TITLE OF INVENTION: DNA COMPRISING RICE ANTER-SPECIFIC GENE AND TRANSGENIC PLANT TRA
 ; FILE REFERENCE: S-30723A
 ; CURRENT APPLICATION NUMBER: US/09/848, 696
 ; CURRENT FILING DATE: 2001-05-03
 ; PRIOR APPLICATION NUMBER: KR 98-46973
 ; PRIOR FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.2
 ; SEQ ID NO 3
 ; LENGTH: 1196
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; US-09-848-696-3
 Query Match 83.3%; Score 1196; DB 9; Length 1196;
 Best Local Similarity 100.0%; Pred. No. 5e-281; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 6
US-10-602-166-3
; Sequence 3, Application US/10602166
; Publication No. US20040060084A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTER-SPECIFIC GENE AND TRANSGENIC PLANT TRA
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/10/602,166
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/848,696
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 3
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-602-166-3

Query Match          83.3%; score 1196; DB 18; Length 1196;
Best Local Similarity 100.0%; Pred. No. 5e-281;
Matches 1196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
1 CATTCTAGTTATCCTCCAGCCTACATGTACTCTCTCCATAATACAAGTGTCTATGA 60
Db
1 CATTCTAGTTATCCTCCAGCCTACATGTACTCTCTCCATAATACAAGTGTCTATGA 60
QY
61 TTCAAATTGTCCTACATATAACATTCCAGCATGAATCCATACATTAATTTCAG 120
Db
61 TTCAAATTGTCCTACATATAACATTCCAGCATGAATCCATACATTAATTTCAG 120
QY
121 CTAATCAGATGCTTGGAGGAAATCTAAGCGATTCAATATGCCAAATGACTGA 180
Db
121 CTAATCAGATGCTTGGAGGAAATCTAAGCGATTCAATATGCCAAATGACTGA 180
QY
181 AGTAACTGAAAGAGAATACTCGTTAACATTAGTGCTTAGTTATAACAACTAA 240
Db
181 AGTAACTGAAAGAGAATACTCGTTAACATTAGTGCTTAGTTATAACAACTAA 240
QY
241 AAATGTTTATTTAGTACAATCGAGTAGCTAGGAGCTAGGTAAGATCG 300
Db
241 AAATGTTTATTTAGTACAATCGAGTAGCTAGGAGCTAGGTAAGATCG 300
QY
301 TGTTCGGATCACCTGAGAACCGTCAAGGTGGTTGTGCTCTGCGCTCCAGCGGATCAGAT 360
Db
301 TGTTCGGATCACCTGAGAACCGTCAAGGTGGTTGTGCTCTGCGCTCCAGCGGATCAGAT 360
QY
361 TCGGAGATCCGGCTGCTGAGAACCGTCAAGGTGGTTGTGCTCTGCGCTCCAGCGGATCAGAT 420
Db
361 TCGGAGATCCGGCTGCTGAGAACCGTCAAGGTGGTTGTGCTCTGCGCTCCAGCGGATCAGAT 420
QY
421 AGCAAGAGCAATGGCGTAGGGAGTTGACTTTGACTAGCTAGTAGGGCG 480
Db
421 AGCAAGAGCAATGGCGTAGGGAGTTGACTTTGACTAGCTAGTAGGGCG 480

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US-09-848-696-10

Query Match 16.7%; Score 240; DB 9; Length 240;

Best Local Similarity 100.0%; Pred. No. 3.4e-48; Mismatches 0; Indels 0; Gaps 0;

Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1197 GCAAAGTCTCAAGGGAAACGCCCTCCATCTCTCAGCTCTCCATGGCGTCCC 1256

Db 1 GCAAAGTCTCAAGGGAAACGCCCTCCATCTCTCAGCTCTCCATGGCGTCCC 60

Qy 1257 TCGTCGCCATGCCATGCCATGGCTCATGGCGAGAGATCCAGCATGTAATT 1316

Db 61 TCGTCGCCATGCCATGCCATGGCTCATGGCGAGAGATCCAGCATGTAATT 120

Qy 1317 AACTTGACGCATATCATCTCATCATCACTTGCAATTCTGGATTTGAGACATG 1376

Db 121 AACTTGACGCATATCATCTCATCATCACTTGCAATTCTGGATTTGAGACATG 180

Qy 1377 TTAGCTGATCAGTAACGTGCGGTGTTGAATTGGCTTATCAGGTGGTCAACCTGG 1436

Db 181 TTAGCTGATCAGTAACGTGCGGTGTTGAATTGGCTTATCAGGTGGTCAACCTGG 240

RESULT 8 US-10-602-166-10

; Sequence 10, Application US/10602166 ; Publication No. US20040060084A1

; GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 87679 ; LENGTH: 712 ; TYPE: DNA ; ORGANISM: Oryza sativa ; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_86601C.1 US-10-437-963-87679

Query Match 7.5%; Score 107.4; DB 19; Length 712; Best Local Similarity 71.4%; Pred. No. 1.3e-15; Mismatches 175; Conservative 0; Mismatches 56; Indels 14; Gaps 2; Matches 175; Conservative 0; Mismatches 56; Indels 14; Gaps 2;

Qy 585 TCTGTTGGAGCTAAATTATGAAAGCAGCTGCTGAGAGCTAGCTGGTGAATCT 644

Db 98 TGTTGGGGAGCTTAAGATTCCTGAGAACGCTGCTGAGAGCTAGCTGGTAAATT 157

Qy 645 GAAGAATTGGAGTCTAC-----GTCATCTCCAGATTACAATTACAGAT 692

Db 158 GGAGAAGCTGGAAAACCCAGCTTCTAGCTPTGTTCAATTCTAGATTCTACAATTACAGAT 217

Qy 693 TCTTATAATTAGTAAAGCTGGACTGTT--GGGAGCTCTGTCAAGCCGGAGATTCT 750

Db 218 TCTTAAATCTAGTAAAGCTTAATTGTTGAGGGAGCTCTGGTAACTGGAGATTCT 277

Qy 751 GTGAGAAGCTGCAGCTGCTGAGACTCCCAAACAGACCCCTAGTTGACTCTAGCTGA 810

Db 278 ATAAGAAGATCTAGCTGCTAGAAGCTCCCTAAACAAAGCCCTAGTATGACTAAACATGA 337

Qy 811 TCGAT 815

Db 338 TCGT 342

RESULT 9 US-10-602-166-10

Query Match 16.7%; Score 240; DB 18; Length 240;

Best Local Similarity 100.0%; Pred. No. 3.4e-48; Mismatches 0; Indels 0; Gaps 0;

Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1197 GCAAAGTCTCAAGGGAAACGCCCTCCATCTCTCAGCTCTCCATGGCGTCCC 1256

Db 1 GCAAAGTCTCAAGGGAAACGCCCTCCATCTCTCAGCTCTCCATGGCGTCCC 60

Qy 1257 TCGTCGCCATGCCATGCCATGGCTCTCATGGCAGAGATAATCCAGCATGCTGAATT 1316

Db 61 TCGTCGCCATGCCATGCCATGGCTCTCATGGCAGAGATAATCCAGCATGCTGAATT 120

Qy 1317 AACTTGACGCATATCATCTCATCACTTGCAATTCTGGATTTGCGAGACATG 1376

Db 121 AACTTGACGCATATCATCTCATCACTTGCAATTCTGGATTTGCGAGACATG 180

Qy 1377 TTAGCTGATCAGTAACGTGCGGTGTTGAATTGGCTTATCAGGTGGTCAACCTGG 1436

Db 181 TTAGCTGATCAGTAACGTGCGGTGTTGAATTGGCTTATCAGGTGGTCAACCTGG 240

RESULT 9

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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-848-696-7

Query Match 6.6%; Score 95; DB 9; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1197 GCAAAGTCTCAAGGGAAACCGCCTCCATCTCTCAGCTCCTCCATGGGTCCC 1256
DB 1 GCAAAGTCTCAAGGGAAACCGCCTCCATCTCTCAGCTCCTCCATGGGTCCC 60

QY 1257 TCGTCGCCATGCCCATGCCATGGCTCATGGTG 1291
DB 61 TCGTCGCCATGCCCATGCCATGGCTCATGGTG 95

RESULT 11
US-10-602-166-7
; Sequence 7, Application US/10602166
; Publication No. US20040060084A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHER-SPECIFIC GENE AND TRANSGENIC PLANT TRA
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/10/602,166
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/848,696
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 7
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-602-166-7

Query Match 6.6%; Score 95; DB 18; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1197 GCAAAGTCTCAAGGGAAACCGCCTCCATCTCTCAGCTCCTCCATGGGTCCC 1256
DB 1 GCAAAGTCTCAAGGGAAACCGCCTCCATCTCTCAGCTCCTCCATGGGTCCC 60

QY 1257 TCGTCGCCATGCCCATGCCATGGCTCATGGTG 1291
DB 61 TCGTCGCCATGCCCATGCCATGGCTCATGGTG 95

RESULT 13
US-10-437-963-72585
; Sequence 72585, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 72585
; LENGTH: 1250
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
NAME/KEY: unsure
LOCATION: (1). (1250)
; OTHER INFORMATION: unsure at all n locations
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72950C.1
; US-10-437-963-72585

Query Match 6.5%; Score 93.4; DB 19; Length 1250;
Best Local Similarity 98.9%; Pred. No. 4.7e-12;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1197 GCAAAGTCTCAAGGGAAACCGCCTCCATCTCTCAGCTCCTCCATGGGTCCC 1256
DB 13 GCAAAGTCTCAAGGGAAACCGCCTCCATCTCTCAGCTCCTCCATGGGTCCC 72

QY 1257 TCGTCGCCATGCCCATGCCATGGCTCATGGTG 1291
DB 73 TCGTCGCCATGCCCATGCCATGGCTCATGGTG 107

RESULT 14
US-10-260-238-2616
; Sequence 2616, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.


```

; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provar, Nicholas
; APPLICANT: Rickie, Darrell
; APPLICANT: Zhu, Tong

TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION

FILE REFERENCE: 60111-NP

CURRENT APPLICATION NUMBER: US/10/260, 238

CURRENT FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: US 60/325, 448

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/370, 620

PRIOR FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 6077

SEQ ID NO 2616

LENGTH: 2000

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

NAME / KEY: N region

LOCATION: (T496)..(1496)

OTHER INFORMATION: n = any nucleotide

US-10-260-238-2616

Query Match 5.4%; Score 77.2; DB 18; Length 17953;
Best Local Similarity 68.3%; Pred. No. 1.8e-07;
Matches 142; Conservative 0; Mismatches 53; Indels 13; Gaps 2;

Query 589 TTGGGAGCTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTAGAATCTGAAG 648
Db 17088 TTGGGGAGCTTAAGATTCTGAGAAGTAGCTGGTAGCTAGCTTCGTATAATCTGGAA 17147

Query 649 AATTGAGTTCTACGTTCAATTCCAGATTCTACAAATTACAGATTCTATAATTAGCTA 708
Db 17148 AAGTTGGTT---TTCACCTCTGGCTTCTATAACTACAGATCTAGAACCTGAGTG 17203

Query 709 AAAAGCTGAGCTTGGAGCTCTGTCAAGCGGAGATTCTGAGAAGCTGCAGCTGC 768
Db 17204 AGAATGTAAGACTATTGAGG-----AGCTGAAATTCTAAAGAAACTGCAAAAC 17254

Query 769 TAGAGCTCCCCAACAGACCCCTAGT 796
Db 17255 TAGAAGCTCAACTCAAACAGGCCCTAGT 17282

Search completed: September 23, 2005, 19:36:05
Job time : 720 sec

RESULT 15
US-10-415-058-4

; Sequence 4, Application US/10415058
; Publication No. US20040060081A1

GENERAL INFORMATION:

APPLICANT: Wisconsin Alumni Research Foundation

APPLICANT: United States Department Of Agriculture

APPLICANT: Leong, Sally A.

APPLICANT: Farman, Mark L.

APPLICANT: Chauhan, Rajinder

APPLICANT: Durfee, Timothy J.

TITLE OF INVENTION: Plant Gene That Confers Resistance To Strains Of Magnaporthe Gris

FILE REFERENCE: Warf-0145

CURRENT APPLICATION NUMBER: US/10/415, 058

CURRENT FILING DATE: 2003-04-11

PRIOR APPLICATION NUMBER: USSN 60/242, 313

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: USSN 60/303, 897

PRIOR FILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 17953
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-415-058-4

Query Match 5.4%; Score 77.2; DB 18; Length 17953;
Best Local Similarity 68.3%; Pred. No. 1.8e-07;
Matches 142; Conservative 0; Mismatches 53; Indels 13; Gaps 2;

Query 589 TTGGGAGCTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTAGAATCTGAAG 648
Db 17088 TTGGGGAGCTTAAGATTCTGAGAAGTAGCTGGTAGCTAGCTTCGTATAATCTGGAA 17147

Query 649 AATTGAGTTCTACGTTCAATTCCAGATTCTACAAATTACAGATTCTATAATTAGCTA 708
Db 17148 AAGTTGGTT---TTCACCTCTGGCTTCTATAACTACAGATCTAGAACCTGAGTG 17203

Query 709 AAAAGCTGAGCTTGGAGCTCTGTCAAGCGGAGATTCTGAGAAGCTGCAGCTGC 768
Db 17204 AGAATGTAAGACTATTGAGG-----AGCTGAAATTCTAAAGAAACTGCAAAAC 17254

Query 769 TAGAGCTCCCCAACAGACCCCTAGT 796
Db 17255 TAGAAGCTCAACTCAAACAGGCCCTAGT 17282

Search completed: September 23, 2005, 19:36:05
Job time : 720 sec

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CM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 16:39:48 ; Search time 197 Seconds
(without alignments)
11927.377 Million cell updates/sec

Title: US-10-602-166-2
Perfect score: 1436
Sequence: 1 cattcagaatcatctccagc.....tatcagggtggtaaaccttg 1436

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 810138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backFiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46.2	3.2	7218	1	US-08-232-463-14
2	44.8	3.1	13158	2	US-08-687-080-105
3	44.6	3.1	832	4	US-09-621-976-2813
4	43.6	3.0	1664976	4	US-08-916-421B-1
5	43.6	3.0	1664976	4	US-09-692-570-1
6	43.4	3.0	1039	4	US-09-902-540-1280
7	42.4	3.0	612	4	US-09-902-540-1357
8	42.4	3.0	740	3	US-08-998-416-563
9	41.8	2.9	570	4	US-09-621-976-1972
10	41.8	2.9	2748	4	US-09-949-016-1448
11	41.8	2.9	36154	4	US-09-949-016-13190
12	40.6	2.8	601	4	US-09-949-016-202462
13	40.4	2.8	6243	2	US-09-056-075-1
14	40.4	2.8	212139	4	US-09-949-016-16065
15	40	2.8	601	4	US-09-949-016-87645
16	40	2.8	19124	2	US-08-487-826B-13
17	40	2.8	670689	4	US-09-949-016-12505
18	40	2.8	670690	4	US-09-949-016-14207
19	39.8	2.8	897	4	US-09-270-767-3490
20	39.8	2.8	897	4	US-09-270-767-18772
21	39.6	2.8	601	4	US-09-949-016-122354
22	39.6	2.8	19124	2	US-08-487-826B-13
23	39.6	2.8	36618	4	US-09-949-016-16935
24	39.6	2.8	45842	4	US-09-949-016-12550
25	39.6	2.8	45842	4	US-09-949-016-17327
26	39.6	2.8	74730	4	US-09-949-016-15189
27	39.4	2.7	601	4	US-09-949-016-91213

Sequence 91214, A
Sequence 166398, A
Sequence 17422, A
Sequence 16423, A
Sequence 14353, A
Sequence 11808, A
Sequence 13388, A
Sequence 122355, A
Patent No. 5231168
Sequence 15092, A
Sequence 202463, A
Sequence 5, Appli
Sequence 3, Appli
Sequence 12528, A
Sequence 12386, A
Sequence 16915, A
Sequence 1, Appli

ALIGNMENTS

RESULT 1	US-08-232-463-14
;	Sequence 14, Application US/08232463
;	Patent No. 5670367
;	GENERAL INFORMATION:
;	APPLICANT: DORNER, F.
;	APPLICANT: SCHEIFLINGER, P.
;	APPLICANT: FALKNER, F. G.
;	TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;	NUMBER OF SEQUENCES: 52
;	CORRESPONDENCE ADDRESS:
;	ADDRESSEE: Foley & Lardner
;	STREET: 1800 Diagonal Road, Suite 500
;	CITY: Alexandria
;	STATE: VA
;	COUNTRY: USA
;	ZIP: 22313-0299
;	COMPUTER READABLE FORM:
;	MEDIUM TYPE: FLOPPY disk
;	COMPUTER: IBM PC compatible
;	OPERATING SYSTEM: PC-DOS/MS-DOS
;	CURRENT APPLICATION DATA:
;	APPLICATION NUMBER: US/08/232,463
;	FILING DATE:
;	CLASSIFICATION: 435
;	PRIOR APPLICATION DATA:
;	APPLICATION NUMBER: US/07/935,313
;	FILING DATE:
;	APPLICATION NUMBER: EP 91 114 300.6
;	FILING DATE: 26-AUG-1991
;	ATTORNEY/AGENT INFORMATION:
;	NAME: BENT, Stephen A.
;	REGISTRATION NUMBER: 29,768
;	REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;	TELECOMMUNICATION INFORMATION:
;	TELEPHONE: (703)835-9300
;	TELEFAX: (703)683-4109
;	TELEX: 899149
;	INFORMATION FOR SEQ ID NO: 14:
;	SEQUENCE CHARACTERISTICS:
;	LENGTH: 7218 base pairs
;	TYPE: nucleic acid
;	STRANDEDNESS: single
;	TOPOLOGY: linear
;	IMMEDIATE SOURCE:
;	CLONE: PT29pt-F1s
;	US-08-232-463-14

Query Match 3.2%; Score 46.2%; DB 1; Length 7218;

Best Local Similarity 6.3%; Pred. No. 0.033; Mismatches 186; Indels 0; Gaps 0; Matches 27; Conservative 218; Mismatches 186; Indels 0; Gaps 0;

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLogy: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 5' END OF INTRON 21 OF RAD50 GENOMIC
INDIVIDUAL ISOLATE: SEQUENCE
US-08-687-080-105

Query Match 3.1%; Score 44.6; DB 2; Length 13158;
Best Local Similarity 52.1%; Pred. No. 0.12; Mismatches 92; Indels 0; Gaps 0;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 920 TTACCGACCTAGTCGGCATTTGAATTAAATAATTAGAGCTGATTTGATT 979
Db 3008 TTAACAAACCATAGCTTTAATGTGAATTGTATTCTTCTCTGAATACTTCATCA 3067

Qy 980 TTTTCAGCGGAATTATTACCGTATGTAAGTTAACCTATAATTATTATT 1039
Db 3068 TCTCATCTGCATTATTCTTTGCTTAATTTAGTTTACCTTGTTTAATCATCA 3127

Qy 1040 CAGGGAGTAGCATTAGTGTATGGTTATAATCATCTGGTATGCTTAATCTCTTAC 1099
Db 3128 CAAATGAGTATAATTATTGTGGTGGTTCTATAAGCCCGATTTCCCAATTCTTGT 3187

Qy 1100 TTGGACTTAGTT 1111
Db 3188 TCATTCTGCTT 3199

RESULT 2
US-08-687-080-105

Sequence 105, Application US/08687080
Patent No. 5965427

GENERAL INFORMATION:

APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

COMPUTER TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 13158 base pairs

RESULT 3
US-09-621-976-2813

Sequence 2813, Application US/09621976
Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pml
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813

Query Match 3.1%; Score 44.6; DB 4; Length 832;
Best Local Similarity 9.3%; Pred. No. 0.027; Mismatches 29; Conservative 154; Mismatches 128; Indels 0; Gaps 0; Matches 29; Conservative 154; Mismatches 128; Indels 0; Gaps 0;

Qy 893 TTGATGTTCTTCATCGTAATTCACCTACCGACCTAGTCGGCATTTGAATTAAA 952
Db 43 KKKKAWKWKWTKWYWRYAMWGYKKAMCRTKTKKKKKGYMMMWGWRSSYMMW 102

Qy 953 ATAATTAGCTAGGCTGATTGATTCTTCAGCGAATTTCACGTAATGTA 1012
Db 103 TRTWIGAYYRSMMWYRCKWKKKAYRKITCYSSKGWTWWKRWKAWTWWKTYW 162

Qy 1013 AAGTTTACCTAAATTTCAGCGGAGTAAGCATAGTGTATGGGTATAA 1072
Db 163 AATRYWMMWCKWRAWSWYCWNGKARKWSTWRKSRSYASAKRCYCSCSWGAMSW 222

Qy 1073 TCATCTGGTATGCTTAATCTCTTACTGGACTTAGTGGACAATTCTGAATGATTC 1132

Db 223 KYMWRMRWWRGATAGAGKSKTSYKSMWCWTRSWKYCYTKARWT 282
QY 1133 TCGGCCATCTCTATAACGCCCTGCTTAGCTTGTACTGCCACACAAGACTA 1192
Db 283 GYYCYRKGGMWGKRGRWYASKKYMWRWWCARMYRSTGTRASMMWRWYTMKWW 342
QY 1193 GCTGGCAAAT 1203
Db 343 KYAWARAAWRW 353

RESULT 4
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191989)..(191989)

; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
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; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (312993)..(312993)
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; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
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; LOCATION: (600092)..(600092)
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; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (682442)..(682442)
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; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (741684)..(741684)
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; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
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; LOCATION: (1349491)..(1349491)
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; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
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; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match 3.0%; Score 43.6; DB 4; Length 1664976;
Best Local Similarity 47.2%; Pred. No. 4;
Matches 202; Conservative 0; Mismatches 219; Indels 7; Gaps 2;

QY 674 AGATTCTACCAATTACAGATTCTATAATTAGGAAAGCTGGACTGTGGAGCTC 733
Db 251603 AGATTAAGCCAAATGGAAAACCTGAACCTAAGGTTAAAAAGGTTATTAGCAAGATAT 251662

QY 734 TGTCAAGCCGAGATTCTGTGAGAACGCTGCAGCTGCTAGAGCTTCCCACAGACCCCT 793
Db 251663 GCTTAAGCTTGAAAGTTCAGCTGTAGGGAGCTGTATTAGATAATAGAGATT 251722

QY 794 AGTTGTACTCTAGCTGATCGATTCTACTCTATTATAACCTGTCTCTAGCTTAC 853
Db 251723 CTTTATGCTTATGTTTACATAATATTATTACCAATTAT--AATTGTCT 251779

QY 854 AACCGTAGCCAAGACTGAAATTAAAGCTTAATTGATTTGATGTCTTCTCATCGTA 913
Db 251780 GTAAACACTAGGACTAGGATTTTAATTATATGGATTGGAAGTTATCTCGTCA 251839

QY 914 ATTCACTTACCGAACCTAGTCGGCATTTAAATAATTTAGAGCTGATT 973
Db 251840 ATACATTATAATTAGGAAACCCATTAAATCTGATATCATTTAACCTTT 251899

QY 974 TGATTTTTTCAGCGGAATTATTTCAGC---TATGAAAGTTACCTATAAT 1029
Db 251900 TATCTAAATTCTAAGGGTAGCTTAAATAATTATTGATTTGATTGTTAAATTA 251959

QY 1030 TATTAATTTCAGCGGAAGCATTAGTGTATGGTTATAATCATCTGGTATGCTAA 1089

RESULT 5
US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US 09/692,570
; PRIORITY APPLICATION NUMBER: US 60/024,428
; PRIORITY FILING DATE: 1996-08-22
; PRIORITY APPLICATION NUMBER: US 08/916,421
; PRIORITY FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (848120)..(848121)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (103998)..(103998)

OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (148⁻948)..(148948)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (163385)..(163385)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (191989)..(191989)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (231980)..(231980)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (234187)..(234187)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (234220)..(234220)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (234814)..(234814)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (309398)..(309398)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (309418)..(309418)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (312837)..(312837)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (312993)..(312993)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (319226)..(319226)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (559167)..(559167)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (559241)..(559241)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (600992)..(600992)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (622708)..(622708)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (657081)..(657081)
 OTHER INFORMATION: n equals a, t, c, or g

FEATURE:
 NAME/KEY: misc feature
 LOCATION: (657⁻203)..(657203)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (674435)..(674435)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (682442)..(682442)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (713652)..(713652)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (741684)..(741684)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (779455)..(779455)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (779676)..(779676)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (855539)..(855539)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (871619)..(871619)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1084830)..(1084830)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1096846)..(1096846)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1119881)..(1119881)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1130881)..(1130881)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1130988)..(1130988)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1313224)..(1313224)
 OTHER INFORMATION: n equals a, t, c, or g
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1349473)..(1349473)
 OTHER INFORMATION: n equals a, t, c, or g

Query Match 3.0%; Score 43.6; DB 4; Length 1664976;
 Best Local Similarity 47.2%; Pred. No. 4; Mismatches 219; Indels 7; Gaps 2;
 Matches 202; Conservative 0; Mismatches 219; Indels 7; Gaps 2;
 QY 674 AGATCTACAATTACAGATCTTATAATTAGTAAAGCTGGACTGTTGGACCTTC 733
 Db 251603 AGATTAGCCAAATGGAACCTGAACCTAAGGTTATTAGCAAGAT 251662

QY 734 TGGCAGCCGGAGATCTGTGAGAAGCTGCAGCTGCTAGAACAGACCCCT 793
Db 251663 GCTTAAGCTTGTAAAGTTCACTGAGCTGATGAGGGAGCTGTATTAGAGATT 251722
QY 794 AGTTGACTCTAGCTGATCGATTCACTCTATTATACACCTTGCTCTAGCTTAC 853
Db 251723 CTTTATGCTTATGTTTACATAATATTACCAATTAT--AATTGTGTC 251779
QY 854 AAACGTTAGCCAAGACTTGAATTAAAGCTTAATTGATTGTGCTTCACTCGTA 913
Db 251780 GTAAATACACTAGGACTAGGATTAAATTATGGATTGGAAGGTTATCTCGTCA 251839
QY 914 ATTCACCTACCGACCTTAGTCGGATTGAAATTAAATAATTAGAGCTGATT 973
Db 251840 ATACATTATAATTAGGAAACCCATTAAATCTGATATCATTATTTAACCTTT 251899
QY 974 TGATTTTCAGCGGAATTATTTCACG---TATGAAAGTTACCTAAAT 1029
Db 251900 TATCTAATTCTAAGGGTAGCTTAAATTAAATTGTTAATTTAATGTTAAATTA 251959
QY 1030 TATTAATTTCAGCGGAGTAAGCTTAGTGTATGGTTATAATCATCTGGTATGCTAA 1089
Db 251960 TAGGGATTTTAAATTCTACTTAATGTTTATTGAGATTCTCCAATGATCAA 252019
QY 1090 ATCTCTT 1097
Db 252020 TTTCATT 252027

RESULT 6

- Sequence 1280, Application US/09902540
- ; Patent No. 6833447
- ; GENERAL INFORMATION:
- ; APPLICANT: Goldman, Barry S.
- ; APPLICANT: Hinkle, Gregory J.
- ; APPLICANT: Slater, Steven C.
- ; APPLICANT: Wiegand, Roger C.
- ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
- ; FILE REFERENCE: 38-10(15849)B
- ; CURRENT APPLICATION NUMBER: US/09/902,540
- ; CURRENT FILING DATE: 2001-07-10
- ; PRIOR APPLICATION NUMBER: 60/217,883
- ; PRIOR FILING DATE: 2000-07-10
- ; NUMBER OF SEQ ID NOS: 16825
- ; SEQ ID NO 1357
- ; LENGTH: 612
- ; TYPE: DNA
- ; ORGANISM: Myxococcus xanthus
- ; FEATURE:
- ; NAME/KEY: unsure
- ; LOCATION: (1).:(612)
- ; OTHER INFORMATION: unsure at all n locations

US-09-902-540-1280/C

Query Match 3.0%; Score 42.4; DB 4; Length 612;
Best Local Similarity 48.3%; Pred. No. 0.097;
Matches 115; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 874 TTTTAAAGCTTAATTGATTTGATGTTCTTTCATCGTAATTACCGACCTAGT 933
Db 437 TTT 378
QY 934 CGGCATTGAAATTAAATAATTTTAGAGCTGATTGATTTTCAGGGAA 993
Db 377 TTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 318
QY 994 TTATTTTCAGGTATGAAAGTTACCTATAATTAAATTTCAGGGAGTAAGCA 1053
Db 317 TTANTTTTTTTTTTTATTATTATTATTATTATTATTATTATTATTATTATT 258
QY 1054 TTAGTTTATGGTTATAATCATCTGGTATGCTTAATCTCTTACTGGACTTAGT .1.11
Db 257 TTT 200

Query Match 3.0%; Score 43.4; DB 4; Length 1039;
Best Local Similarity 45.5%; Pred. No. 0.068;
Matches 155; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

RESULT 8

- Sequence 563, Application US/08998416
- ; Patent No. 6239264
- ; GENERAL INFORMATION:
- ; APPLICANT: Philippson, Peter
- ; APPLICANT: Pohlmann, Rainer
- ; APPLICANT: Steiner, Sabine
- ; APPLICANT: Mohr, Christine
- ; APPLICANT: Wendland, Jurgen
- ; APPLICANT: Knechtle, Philipp
- ; APPLICANT: Reischung, Corinne
- ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHYA GOSSYPII
- ; TITLE OF INVENTION: AND USES THEREOF
- ; NUMBER OF SEQUENCES: 1152

QY 796 TTGTACTCTAGCTGATCGATTCACTTATTATACACCTGCTCTAGCTTCAA 855
Db 375 TTGTTTTTTTGTATTATTAAATTTTTATTGATTGATTTAATTTTTT 316
QY 856 ACGTAGCCAAGACTTGAATTAAAGCTTAATTGATTGATGTTCTTCATCGTAAT 915
Db 315 TTTTATTTTTTTTTGATTTTTATTATTATTATTATTATTATTATTATT 256
QY 916 TCACTACGCCACTAGTCGGCATTTGAATTAAATAATTTAGAGCTGATTTG 975
Db 255 TGTGTTTTTATATTATTATTATTATTATTATTATTATTATTATTATTATT 196
QY 976 ATTTCAGGGATTATTICACGTATGTAAGTTTACTATAATTAA 1035

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 563:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1390RP
; US-08-998-416-563

Query Match 3.0%; Score 42.4; DB 3; Length 740;
Best Local Similarity 49.1%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 814 ATTCACTCTATTATACACCTTGCTCTCTAGCTTATCAAACGTTAGCCAAAGACTTGAA 873
Db 106 ATTATTTGATTGTGACATTGTGATATGTTAAATAATTAA 165

Qy 874 TTAAAGCTTAATTGATTGATTGTTGATGTTCTTCATCGTAATTCACTTACCGACCTAGT 933
Db 166 TATTATTTATAATTATTATTATCTAGTCAGCTCATATAATATGAATAT 225

Qy 934 CGGCATTGGATTAAATAATTAGGTGATTGTGTTTCAGGGAA 993
Db 226 TCCATTATTAAATTGTTAGGATAAACATAATTAAATAACTTATTAAAGTTCAA 285

Qy 994 TTATTTACGTATGTAAGTTACCTATAATTAAATTAAATTCA 1041
Db 286 TAATATGTCTATTTATGATTAATTCAACGTTACGATATAA 333

RESULT 9
US-09-621-976-1972
Sequence 1972, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1972

RESULT 11
US-09-949-016-13190
Sequence 13190, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

LENGTH: 570
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 92..340
NAME/KEY: sig_peptide
LOCATION: 92..325
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 3.7000004768372
OTHER INFORMATION: seq NLITAFSSPSTS/TP
US-09-621-976-1972

Query Match 2.9%; Score 41.8; DB 4; Length 570;
Best Local Similarity 61.5%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 940 TTGATTTTAAATAATTAGGCTGATTGATTTTCAGGGAAATTATT 999
Db 390 TTGAAATTATAATATGTTAGGAATTCTAGGATTTTACCGCTTAC 449

Qy 1000 TTCACCTATGTAAGTTACCTATAATTAAATTATTCAGGGAGT 1048
Db 450 GACCCAATGTAATATTAAATAATTGCAATTCTACAGAAT 498

RESULT 10
US-09-949-016-1448
Sequence 1448, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1448
LENGTH: 2748
TYPE: DNA
ORGANISM: Human
US-09-949-016-1448

Query Match 2.9%; Score 41.8; DB 4; Length 2748;
Best Local Similarity 61.5%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 940 TTGATTTTAAATAATTAGGCTGATTGATTTTCAGGGAAATTATT 999
Db 2582 TTGAAATTATAATATGTTAGGAATTCTAGGATTTTACCGCTTAC 2641

Qy 1000 TTCACGTATGTAAGTTACCTATAATTAAATTATTCAGGGAGT 1048
Db 2642 GACCCAATGTAATATTAAATAATTGCAATTCTACAGAAT 2690

RESULT 11
US-09-949-016-13190
Sequence 13190, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13190
; LENGTH: 36154
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13190

Query Match 2.9%; Score 41.8; DB 4; Length 36154;
Best Local Similarity 61.5%; Pred. No. 1.5; Mismatches 0; Indels 42; Gaps 0;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 940 TTGAATTAAAATATTAGAGCTGATTGATTTCAGCGGAATTATT 999
Db 33988 TTGAAATTATAATATGTATGAAATTCTTAGGATTTTACAGCTTGTACA 34047

Qy 1000 TTCAAGTATGAAAGTTACCTATAATTAAATTTCAGGGACT 1048
Db 34048 GACCCAATGTAATTAATTAATTGCAATTCTACAGAAT 34096

RESULT 12
US-09-949-016-202462/c
Sequence 202462, Application US/09949016
; PATENT NO. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202462
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-202462

Query Match 2.8%; Score 40.6; DB 4; Length 601;
Best Local Similarity 48.4%; Pred. No. 0.31; Mismatches 115; Indels 0; Gaps 0;
Matches 109; Conservative 1; Mismatches 115; Indels 0; Gaps 0;

Qy 40 ATATAACAAGTGTCTATGATTCAAAATTGTCTACAATATAACATTCCAGCATGA 99
Db 347 ATACAAAGCATCTGCATATATTAGGTCTCACTAAATGTAACYAGCATCATTAA 288

Qy 100 AATCCATACATAATTTCAGCTAACATCAGTCTGGAGGAAATCTAAGCGATCAA 159
Db 287 GATACAAATAAACATTGAGTACAGGGATTAGCAGTTACAAATATTGTATA 228

Qy 160 TATGCCAAAATGATCACTGAAGTAATCTCGTTAACATTAGTGCT 219
Db 227 AGAGTATATGTAATTGTAAATTAAATAAGTGTTAAATTAAATTAGGRT 168

Qy 220 AGTATTATAACAACATAAAATTGTTATTTAGTACAA 264
Db 167 AAATTCAAGAAAAAGTAAATACAGGCACTCTAACGACACA 123

RESULT 13
US-09-056-075-1
; Sequence 1, Application US/09056075
; PATENT NO. 5955368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marite
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; TELECOMMUNICATION INFORMATION:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
; ; OTHER INFORMATION: plasmid RP4"
; US-09-056-075-1

Query Match 2.8%; Score 40.4; DB 2; Length 6243;
Best Local Similarity 49.1%; Pred. No. 1.3; Mismatches 111; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 40 ATATAACAAGTGTCTATGATTCAAAATTGTCTACAATATAACATTCCAGCATGA 99
Db 1227 ATAAAAAATAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 1286

Qy 100 AATCCATACATAATTTCAGCTAACATCAGTCTGGAGGAAATCTAAGCGATCAA 159
Db 1287 AAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 1346

Qy 160 TATGCCAAAATGATCACTGAAGTAATCTCGTTAACATTAGTGCT 219
Db 1347 AATATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 1406

Qy 220 AGTATTATAACAACATAAAATTGTTATTTAGTACAA 257
Db 1407 TTTTTTATTAAGTTGAAAAATTTTTATTA 1444

RESULT 14
US-09-949-016-16065

Sequence 16065, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 16065

; LENGTH: 212139

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-16065

Query Match 2.8%; Score 40; DB 4; Length 601;
Best Local Similarity 49.1%; Pred. No. 0.46; Mismatches 110; Indels 0; Gaps 0;

Matches 106; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Db	203 GCTTAACTCTGCCCTGGAACCTTGTCTATCCCTGCTTACTGTCCTAAGAGCCT 262
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Qy	1001 TCACGTATGAAAGTTACCTATAATTATTATTCAGCGGAGTAAGCATTAGTGT 1060
Db	323 TCATATTGTTGAATAACCAAGACACAGCTCTACACTTGGGTTCTGCAGGA 382
Qy	1061 TATGGTTATAATCCTGGTATGCTTAATCTCTT 1096
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US-09-949-016-16065

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Best Local Similarity 47.9%; Pred. No. 10; Mismatches 116; Conservative 0; Indels 0; Gaps 0;

Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

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Qy	870 TGAATTAAAGCTTAATGATTGATTTGATGTTCTCATCGTAATTCACTTACCGACCT 929
Db	51275 ATACAAATGCTGTAAATTAGCTATTATGATTATTGTATTATTGT 51334
Qy	930 TAGTCGGCATTGTAATTAAATAATTAGCTGATTGATTTTCAGC 989
Db	51335 TTGTTGTTTTAAATTTCCTGAATTATATTATGTTGTTGTTGTTACTTT 51394
Qy	990 GGAATTATTTCACGTATGTAAGTTACCTATAATTAAATTTCAGGGAGTA 1049
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RESULT 15

US-09-949-016-87645

; Sequence 87645, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 87645

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-87645

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Beur. S
10/602/66 Page 1
Seq. ID 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 14:46:25 ; Search time 4312 Seconds
(without alignments)
16136.756 Million cell updates/sec

Title: US-10-602-166-2

Perfect score: 1436

Sequence: 1 cattcagaatcatctccagc.....tatcagggtggtaaacctgg 1436

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	1436	100.0	1436	6 BD242728	RESULT 1 BD242728 LOCUS DEFINITION DNA containing rice anther-specific gene and transgenic plants transformed thereby. BD242728
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3	1303	90.7	145828	8 AP005392	transformed thereby.
4	1303	90.7	154188	8 AP005633	BD242728.1 GI:33052498
5	1196	83.3	1196	6 BD242729	JP 2002528125-A/2.
6	1079.8	75.2	2757	8 AF042275	Patent: JP 2002528125-A 2 03-SEP-2002;
7	240	16.7	240	6 BD242735	SYNGENTA PARTICIPATIONS AG
8	184.6	12.9	598	8 AK109240	COMMENT OS Oryza sativa (rice)
9	137.8	9.6	127952	8 OSJN0063	REFERENCE PN JP 2002528125-A/2
10	137.8	9.6	156002	8 OSJN0050	PD 03-SBP-2002
11	127.4	8.9	126544	8 AP005106	PR 02-NOV-1999 JP 2000579761
12	126	8.8	156649	8 AC144738	PI GYNHEUNG AN, JONG SEONG JEON, YOUNG YOUNG CHUNG, SICHOL LEE PC
13	121.6	8.5	195209	2 AP004323	CC DNA containing rice anther-specific gene
14	121.6	8.5	187273	8 AP005966	and transgenic plants
15	120	8.4	134159	2 AP003625	CC transformed
16	120	8.4	168253	8 AP003686	CC thereby
17	118.8	8.3	139421	8 AC087545	FH Key
18	118.8	8.3	300029	8 AE017097	FT source Location/Qualifiers
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FEATURES

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Db	121	CTAATCAGATGCTGGAGGAAAAATCTAACGGATCAATATGATCACTGA	180	Db	1201	AGTCCTCAAGGGAAACCGCTCCATCTTCTCCTCCAGCTCTCCATGGGTCCTCGT	1260
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QY	421	ACCAAGAGCAATGGCGTGCAGGGAGTTGATACTTGACTAGTAGCTAGGGC	480	QY	13.21	TGACGCATATCATCTCATCACTTGCAACTTCTGGATTGTCAGACATGTTA	1380
Db	421	ACCAAGAGCAATGGCGTGCAGGGAGTTGATACTTGACTAGCTAGGGC	480	Db	1321	TGACGCATATCATCTCATCACTTGCAACTTCTGGATTGTCAGACATGTTA	1380
QY	481	TTCGTTCCATGTGCTCTACGCCGTGCGAATGTGCCATGATCCTGATCATGCC	540	QY	13.21	TGACGCATATCATCTCATCACTTGCAACTTCTGGATTGTCAGACATGTTA	1380
Db	481	TTCGTTCCATGTGCTCTACGCCGTGCGAATGTGCCATGATCCTGATCATGCC	540	Db	1321	TGACGCATATCATCTCATCACTTGCAACTTCTGGATTGTCAGACATGTTA	1380
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QY	1021	CCTATAATTATTAATTTCAGCGGAGATTTCAGCTATGTAATTAAAGTTA	1080	QY	1081	TATGCTTAATCTCTTACTGGACTAGTGGACAATCGTAATGCATTCTCGTGC	1140
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A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative', and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene

COMMENT
On Jul 27, 2004 this sequence version replaced gi:49169760. Genes were predicted from the integrated results of the following: GENSCAN (<http://CCR-081.mit.edu/GENSCAN.html>), FGENESH (<http://www.softberry.com/>), Genemark.hmm (<http://www.tigr.org/software/gemmark/>), GlimmerM (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM (<http://rgp.dna.affrc.go.jp/RiceHMM/>), SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor)), sim4 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), sim4 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), gap2 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor) (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (<http://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant protein database, nr (<http://rgp.dna.affrc.go.jp/>). BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative', and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene

COMMENT
On Jul 27, 2004 this sequence version replaced gi:49169760. Genes were predicted from the integrated results of the following: GENSCAN (<http://CCR-081.mit.edu/GENSCAN.html>), FGENESH (<http://www.softberry.com/>), Genemark.hmm (<http://www.tigr.org/software/gemmark/>), GlimmerM (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM (<http://rgp.dna.affrc.go.jp/RiceHMM/>), SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor)), sim4 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), sim4 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), sim4 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), gap2 (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor) (http://rgp.dna.affrc.go.jp/RiceHMM/_SplicePredictor), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (<http://rgp.dna.affrc.go.jp/>). BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative', and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene

predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from SP6 to T7 of the PAC clone.

This sequence of P0463D04 has an overlap with P0463G11(DDBJ:

AP005633) clone at 5' end and with

OSJNBA0087J09(DDBJ: AC108761) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at

<http://rgp.dna.affrc.go.jp/Genomeseq.html>.

FEATURES

source

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Location/Qualifiers

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mRNA

gene

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mRNA

gene

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Best Local Similarity	97.5%; Pred. No. 6.8e-294;
Matches 1409; Conservative	0; Mismatches 25; Indels 11; Gaps 8;
DB	63845 TTAGGCTGATTGATTTTCAGGGAAATTTCACGTATGTAAGTTA 63904
Qy	961 TAGGCTGATTGATTTTCAGGGAAATTTCACGTATGTAAGTTA 1020
Db	1021 CCTATAATTAAATTTCAGGGAGTAGCATAGTGTATATCATCTGG 1080
Qy	63905 CCTATAATTAAATTTCAGGGAGTAGCATAGTGTATATCATCTGG 63904
Db	1081 TATGCTT-AAATCTTACTGGACTTAGTTGGACAAATCGTAATGCATTCTCGTG-C 1138
Qy	63965 TATGCTTAAATCTCTTACTGGACTTAGTTGGACAAATGCATTCTCGTG 63964
Db	1139 CATCTCTT-AATACGGCCTGCTAGCTTGCTCTTGTATCTGCACACAAGAACAGTAGCTGG 1197
Qy	64025 CATCTCTTAAATACGGCCTGCTAGCTTGCTCTTGTATCTGCACACAAGAACAGTAGCT-G 64024
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Qy	63006 CTAATCAGATGCTGGAGGGAAAATCTAAGGATTCAATATGCCAAATGCA 63065
Db	181 AGTAACTGAAAGAGAATATCTCGTTAACATTAGTGTAGTATTAAACAACTAA 240
Qy	63066 AGTAACTGAAAGAGAATATCTCGTTAACATTAGTGTAGTATTAAACAACTAA 63125
Db	241 AAATGTTTATTTAGTACAATCGAGTAGCTGTTAACATTAGTGTAGTATTAAACAACTAA 300
Qy	63126 AAATGTTTATTTAGTACAATCGAGTAGCTGTTAACATTAGTGTAGTATTAAACAACTAA 63125
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Qy	63186 TGTTCCGATCACCTGAGAACCGTCAGGTGGTTGTCAGCAGAGATCG 63245
Db	361 TCGGAGATCCGGCTCGTTTCTGAATTCGAAGTCCCAGCAGCAGCAGCAG 420
Qy	63246 TCGGAGATCCGGCTCGTTTCTGAATTCGAAGTCCCAGCAGCAGCAG 63305
Db	421 AGCAAGAGCAATGGCTGCAAGGAGTTGATACCTTGCACTAGCTACTAGGG 480
Qy	63306 AGCAAGAGCAATGGCTGCAAGGAGTTGATACCTTGCACTAGCTACTAGGG 63365
RESULT 4	AP005633
LOCUS	AP005633
DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9, PAC clone:P0463G11.
ACCESSION	AP005633
VERSION	AP005633.3 GI:50726137
KEYWORDS	Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartooideae; Oryzeae; Oryza. 1
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Sasaki,T., Matsumoto,T. and Katayose,Y.
AUTHORS	clone:P0463G11
TITLE	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
JOURNAL	Published Only in Database (2002)
REFERENCE	2 (bases 1 to 154188)
AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE	Direct Submission
JOURNAL	Submitted (07-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
COMMENT	Gene was predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), GlimmerM (http://www.tigr.org/tab/glimmerm/glmr_form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2
Qy	781 CAAACAGACCCCTACTGTCAGCCGAGATCTGTGAGAAGCTGAGCTTGCAGCTTGC 840
Db	63605 GTTGTGGAGCTCTGTGAGAAGCTGAGCTTGCAGCTTGCAGCTTGC 63664
Qy	841 TCTCTAGCTTACAAACGTAGCTGATTCACTTATACACCTTG 900
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Qy	901 TCTTTCTATCGTAATTCACTTACCGACCTAGTCGGATTAAAGCTTA 960
Db	63665 CAAACAGACCCCTACTGTCAGCCGAGATCTGTGAGAAGCTGAGCTTGC 63724

genomic sequence was searched against NCBI NonRedundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0463G11 has an overlap with P0556A05 (DDBJ: AP005759) clone at 5' end and with P0463D04 (DDBJ: AP005392) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

FEATURES

source

Location/Qualifiers

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misc_feature

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PD	03-SEP-2002	Db	781 CAAACAGACCCCTAGTTGTAICTCTAGCTGATCGATTCACTCTATTATAACCTTGC 840	
PF	02-NOV-1999 JP 2000579761	QY	781 CAAACAGACCCCTAGTTGTAICTCTAGCTGATCGATTCACTCTATTATAACCTTGC 840	
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CC	thereby transformed	Db	841 TCTCTAGCTTATCAAACGTCAGCCAAAGCTGAATTAAAGCTTAATGATTGT 900	
FH	Key source	QY	901 TCTTTTCATCGTAACTCACTTACCGAACCTAGTCGGCATTTGAATTAAAGTTA 960	
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QY	301 TGTTCGGATCACCTGAGAACCGTCAGGTGGTTGTCTGTGCGGTCAAGCGATCAGAAT 360	SOURCE	Oryza sativa	
Db	301 TGTTCGGATCACCTGAGAACCGTCAGGTGGTTGTCTGTGCGGTCAAGCGATCAGAAT 360	ORGANISM	Oryza sativa	
QY	361 TCGGAGATCGCCGTGCGTTCTTCTGAATCTGCAACTCCAGCAGCAGCAGCAG 420	REFERENCE	Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	
Db	361 TCGGAGATCGCCGTGCGTTCTTCTGAATCTGCAACTCCAGCAGCAGCAGCAG 420	AUTHORS	1 (bases 1 to 2757)	
QY	421 AGCAAGAGCAATGGCGTGCAGGGAGTTGATCTGCACTAGCTACTAGGG 480	TITLE	Jeon,J.S., Chung,Y.Y., Lee,S., Yi,G.H., Oh,B.G. and An,G.	
Db	421 AGCAAGAGCAATGGCGTGCAGGGAGTTGATCTGCACTAGCTACTAGGG 480	JOURNAL	Isolation and characterization of an anther-specific gene, RAB, from rice (<i>Oryza sativa</i> L.)	
QY	481 TTGGTCCATGTGCGCTCACGCCGTGCGAATGTGCCATGATCGATCATCGCC 540	MEDLINE	Plant Mol. Biol. 39 (1), 35-44 (1999)	
Db	481 TTGGTCCATGTGCGCTCACGCCGTGCGAATGTGCCATGATCGATCATCGCC 540	PUBMED	99178792	
QY	541 AGGATTATTCCTCACATTTCCTATCGCTCTAGTCGTCTGTTGGAGCTTA 600	REFERENCE	2 (bases 1 to 2757)	
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QY	601 ACGTTCATTCAGATCTACAATTACAGATCTATAATTAGTAAAGCTGGACT 660	TITLE	Direct Submission	
Db	601 ACGTTCATTCAGATCTACAATTACAGATCTATAATTAGTAAAGCTGGACT 660	JOURNAL	Submitted (11-JAN-1998) Life Science, Pohang University of Science and Technology, Pohang 790-784, Republic of Korea	
QY	661 ACGTTCATTCAGATCTACAATTACAGATCTATAATTAGTAAAGCTGGACT 720	FEATURES	Location/Qualifiers	
Db	661 ACGTTCATTCAGATCTACAATTACAGATCTATAATTAGTAAAGCTGGACT 720	source	1. .2757 /organism="Oryza sativa" /mol_type="genomic DNA" /db_xref="taxon:4530" /clone="RA8"	
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ORIGIN	Query Match Best Local Similarity 99.8%; Conservative 0; Matches 1081; Mismatches 2; Indels 0; Gaps 0;	Score 1079.8; DB 8; Length 2757;	polyA_signal	2662. . 2666	
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DB	108 TCGAATTGGAGATCCGCCGCTCTTCTGAATCTGCAGGCCAGCAGCA	167	DB	1068 ATTACTGACCATATCTCATCATCACTTGCACTTGTGAGATGTCAGAC	1127
QY	414 GCAGCAGAGCAAGAGCAATGGGGCAGGGAGTTGATACTTGATGCACTAGCTA	473	QY	1374 ATGTTAGCTGATCAGTAACGTTGCCGTTGATGGCTTATCAGGGGTTCAACC	1433
DB	168 GCAGCAGAGCAAGAGCAATGGGGCAGGGAGTTGATACTTGATGCACTAGCTA	227	DB	1128 ATGTTAGCTGATCAGTAACGTTGCCGTTGATGGCTTATCAGGGGTTCAACC	1187
QY	474 CTAGGGGTCTGGTCCATGTGCGCTCACGCCGCGGAATGTGCCATGCTGATGCAT	533	QY	1434 TGG 1436	
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QY	594 GAGCTAAATTATGAAAGCAGCTGCTGAGAACGAGCTAGCTGGTAGAAATT	653	QY	1377 TTGACTGATCAGTAACGTTGCCGTTGATGGCTTATCAGGGTCAACCTGG	1436
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QY	654 GAGTTCTACGTTCATTCAGATCTCACAAATTACAGATTCTATATTAGTAAAG	713	QY	1197 GCAAAGTCTCAAGGGAAACGCCCTCATCTTCTCCAGCTCCTCCATGGGTC	1256
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QY	714 CTGGACTGTGGAGCTCTGTCAGCCGGAGATTCTGTGAGAACGAGCTGCTAGAA	773	QY	1257 TCGTCGCCATGCCATGCCATGGCTCTCATGGCAGAGATATCCAGCATGCTGAATT	1316
DB	528 GCTTCCCCAACAGACCCCTAGTGTACTCTAGCTGATTCTTACCTTATAC	587	DB	61 TCGTCGCCATGCCATGCCATGGCTCTCATGGCAGAGATATCCAGCATGCTGAATT	120
QY	834 ACTTGCTCTAGCTTACAACGTAAGCTTAAAGCTTAATTGATT	893	QY	1194 CTCGCAAAGTCCTCAAGGGAAACGCCCTCATCTTCCAGCTCCTCCATGGGTC	1253
DB	588 ACCTTGCTCTAGCTTACAACGTAAGCTTAAAGCTTAATTGATT	647	DB	948 CTGGCAAAGTCCTCAAGGGAAACGCCCTCCATCTTCCAGCTCCTCCATGGGTC	1007
QY	894 TTGATGTTCTTCATCGTAATTCACTTACCGACCTAGTCGGCATTTGAA	953	QY	1254 CCCTCGTCGCCATGCCATGCCATGGCTCTCATGGCAGAGATATCCAGCATGCTGAATT	1313
DB	648 TTGATGTTCTTCATCGTAATTCACTTACCGACCTAGTCGGCATTTGAA	707	DB		
QY	954 ATATTTCAGCTGATTTCAGCGACCTAGTCGGCATTTGAA	1013	QY		
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DB	768 AGTTTACCTATAATTATTTCAGCGAGCTAGTCGGCATTTGAA	827	DB		
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DB	828 CATCTGGTATGCTTAATCTCTTACTTGGACTTAGTTCGGACAAATTGTAATGCACT	887	DB		
QY	1134 CGTGCCTACCTCTATAATTACGGCCTGCTAGCTTGCTCTGTATCTGCACACAGACTAG	1193	QY		
DB	888 CGTGCCTACCTCTATAATTACGGCCTGCTAGCTTGCTCTGTATCTGCACACAGACTAG	947	DB		
QY	1194 CTCGCAAAGTCCTCAAGGGAAACGCCCTCATCTTCCAGCTCCTCCATGGGTC	1253	QY		
DB	948 CTGGCAAAGTCCTCAAGGGAAACGCCCTCCATCTTCCAGCTCCTCCATGGGTC	1007	DB		
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RESULT 8	Oryza sativa (japonica cultivar-group) cDNA clone:002-156-F12, full insert sequence.	
ACCESSION	AK109240	598 bp mRNA linear PLN 24-JUL-2003
LOCUS	AK109240	Oryza sativa (japonica cultivar-group) cDNA clone:002-156-F12, full insert sequence.
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:002-156-F12, full insert sequence.	
VERSION	AK109240	FLICDNA; oligo capping.
SOURCE	Orzya sativa (japonica cultivar-group)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
KEYWORDS		
ORGANISM		
REFERENCE		
AUTHORS		The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,B., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
TITLE		Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL	Science 301 (5631), 376-379 (2003)	
PUBMED	12869764	
REFERENCE		
AUTHORS		Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Immamura,K., Imottani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosoaki,T., Kubumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Tagami,A., Tagami-Takeda,Y., Tagami,M., Tagami,T., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
FEATURES		
source		Location/Qualifiers
ORIGIN		
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Db	60 CTCCCATGGCTCCCTGTCGCATCGCCATCGGCATGGCTCATCTGCAGAGGAT	59
QY	1242 CTCCCATGGCTCCCTGTCGCATCGCCATCGGCATGGCTCATCTGCAGAGGAT	1301
Db	1 CACAGAACTAGCT-GCAAAGTCTCAAGGGAACGGCCTCATCTGCAGAGGAT	119
QY	1302 C---AGCATGTCGAATTAACTGACGCATATCATCTCATCATCACTTGCAATTCACT	1357
Db	60 CTCCCATGGCTCCCTGTCGCATCGCCATCGGCATGGCTCATCTGCAGAGGAT	120
QY	1358 TCTGGATGTGCAAGCATGTTAGCTGAT-CAGTAACGTTGCCGTGTGAATTGGCT	1416
Db	180 TCTGGATGTGCAAGCATGTTAGCTGCACTAACGTTGCCGTGTGAATTGGCT	239
QY	1417 T-ATCAGGTGTTAACCTGG	1436
Db	240 TGATCAGGTGTTAACCTGG	260
RESULT 9		
LOCUS	OSJN0063/c	127952 bp DNA linear PLN 10-FEB-2004
DEFINITION	OSJN0063	Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNB0086G13, complete sequence.
ACCESSION	AL606706	
VERSION	AL606706.3	GI:32480089
KEYWORDS		
SOURCE		
ORGANISM		
COMMENT		This clone is one of the 28K full-length cDNA clones from japonica rice.
URL		http://cdna01.dna.affrc.go.jp/cDNA/
		NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
REFERENCE	1	
AUTHORS	Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W.Q., Gu,W.Q., Zhu,G.F., Tu,Y.P., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H., Chen,X.Y., Shao,Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,W.,	

		REFERENCE	Ehrhartoideae; Oryzeae; <i>Oryza</i> .
1	AUTHORS	Feng, Q., Zhang, Y., Hao, P., Wang, S., Fu, G., Huang, Y., Li, Y., Zhu, J., Liu, Y., Hu, X., Jia, P., Zhang, Y., Zhao, Q., Ying, K., Yu, S., Tang, Y., Weng, Q., Zhang, L., Lu, Y., Mu, J., Lu, Y., Zhang, L.S., Yu, Z., Fan, D., Liu, X., Lu, T., Li, C., Wu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan, J., /db_xref="UniProt/TREMBL:Q7X606"	
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	VVSEGVRIWLSSEDGTGAYVFAFPGPQLFHNYTSQAMNREYTSEFRRVNDTLCELVPG	MQIATDIICFFPGTDEDFSQTNLVKQYLFPQWHISQFYPYRPGTPARMKKVPSVEV	
	KRSRELTSVFEFSPYQGMEGKVERIWITEIATDCVHLIGHTKGYIQVLVIAPDSML	GTSADVKITSVGRWSVFGEVTEGSSVAKETOHKHSELOEEYRPSQVEATCCGTDSC	
	GACTCSDAQOCNCNPGRPERSENSTPQSCGDATHQBAVOSKLVRNNVEGAVKSSRSDTA	QVGEIQRLNVAARRFPDVDTILMGGLAGVSPATTTVLIALLAYKISSTPSY"	
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	VEYEREPFLYPLPGDAVKGAVRKCKDRLLGARRAEGKEKASAKESATGKVFKVETAVGAOKVSEAGKAKERASHVHOHGAETVNAKDVKVSH	AKELIARDKVFDAAASKVETAVGAOKVSEAGKAKERASHVHOHGAETVNAKDVKVSH	
	AARHARESARERAMDAKDRVSDDAERAEOCTEDAGRRAAKQAARABEAVKAKAGEAEAS	NLSDIARRARDVDSAADAHLLLGGPREARTATAVMHLLGFAAYGASLWTFVSSYY	
	LAAALPROQIAMLVOSKLFPMYFRAVAYGVGLALAHLGRERSLAARAQSVLAL	ALVLANMLLIEPKATKVMFERMKVEKEBGRGRDMADIIVDPPTVTVAAGNTATTTVPT	
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ACCESSION	AL606626	VERSION	AL606626..3 GI:32488551
KEYWORDS	HTG.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	gene		
		PUBMED	12447439
		REFERENCE	2
		AUTHORS	Fu, G., Wang, S.Y., Ren, S.X., Lv, G., Lin, W., Gu, W.Q., Zhu, G.F., Tu, Y.F., Jia, J., Yin, H.F., Zhang, Y., Cai, Z., Chen, J., Kang, H., Chen, X.Y., Shao, Y., Sun, Y., Hu, Q.P., Zhang, X.L., Zhang, W., Wang, L.J., Ding, C.W., Sheng, H.H., Gu, J.L., Chen, S.T., Ni, L., Zhu, F.H., Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P.X., Oian, Y.M., Ying, K., Zhou, B., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R.Q., Guan, J.P. and Hong, G.F.
		TITLE	Submitted (08-SEP-2001) Han Bin, National Center for Gene Research, Chinese Academy of Sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests: bhan@ncgr.ac.cn
		JOURNAL	
		REMARK	Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC clone: OSJNBA0088K19. On Jul 9, 2003 this sequence version replaced gi:21740748. Web site: http://www.ncgr.ac.cn
		COMMENT	----- Summary Statistics ----- Assembly program: Phrap
			This is a complete sequence.
			Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan (http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (http://genemark.biologics.gatech.edu/Genemark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI non-redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR. Location/Qualifiers
		FEATURES	1. .156002
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gene complement (14232..20388)

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CDS complement (Join(14232..15623,15786..17157,17234..17934,18034..19130,19302..20388))

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RESULT 11

AP05106/c	LOCUS	DEFINITION	VERSION
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		BAC clone:OSJNBb0091119.	

LOCUS AC144738
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 5 clone
ACSJNBa0029B02, complete sequence.
AC144738
VERSION AC144738.2 GI:40385890
KEYWORDS HTG.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 156649)
AUTHORS Chow, T.-Y., Hsing, Y.-I.C., Chen, C.-S., Chen, H.-H., Liu, S.-M.,
Chao, Y.-T., Chang, S.-J., Chen, H.-C., Chen, S.-K., Chen, T.-R.,
Chen, Y.-L., Cheng, C.-H., Chung, C.-I., Han, S.-Y., Hsiao, S.-H.,
Hsiung, J.-N., Hsu, C.-H., Huang, J.-J., Kau, P.-I., Lee, M.-C.,
Leu, H.-L., Li, Y.-F., Lin, S.-J., Lin, Y.-C., Wu, S.-W., Yu, C.-Y.,
Yu, S.-W., Wu, H.-P. and Shaw, J.-P.

mRNA Oryza sativa BAC OSJNBa0029B02 genomic sequence
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gene complement (36502..36711)
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predicted by GlimmerM
this category is not included in IRGSP standard"

Query Match 8.9%; Score 127.4; DB 8; Length 126544;
Best Local Similarity 79.6%; Pred. No. 7.7e-19;
Matches 179; Conservative 0; Mismatches 36; Indels 10; Gaps 2;

QY 576 TCTTAGTCGTCGTGGAGCTTAATTATGAAAAGCAGCTGCTGAGAACCTAGCTGG 635
Db 72464 TCTTAGGGCCAGTTGGGGAGCTTAATTCTGAGAGAGCTGCTGAGAGCTAGCTGG 72405
QY 636 TGAGAAATCTGAAGAATTGAGTTCTACGTTCTACGATTCTACAATTACAGATTCT 695
Db 72404 TGAGAAATCTCTGTCTTCTA-----GTTCATTTTGAGATTCTACAACTAGATTCT 72352
QY 696 TATAATTAGTTAAAGCTGGACTGTT--GGGAGCTCTGTCAAGCCCCAGATTCTGT 752
Db 72351 CGGAATTGGTTAAAGCTGGATGTTGGGGAGCTCTAGCAACTGAAGATTCTAG 72292
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AP004323/c	AP004323	AP005966/c	AP005966
LOCUS	Oryza sativa (japonica cultivar-group) chromosome 6 clone OJ118_C02, *** SEQUENCING IN PROGRESS ***.	LOCUS	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, BAC clone:B1047H05.
DEFINITION	Oryza sativa (japonica cultivar-group) chromosome 6 clone OJ118_C02, *** SEQUENCING IN PROGRESS ***.	DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, BAC clone:B1047H05.
ACCESSION	AP004323	ACCESSION	AP005966
VERSION	AP004323.1	VERSION	AP005966.3
KEYWORDS	HTG; HTGS PHASE2.	KEYWORDS	HTG; HTGS PHASE2.
SOURCE	Oryza sativa (japonica cultivar-group)	SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1	REFERENCE	Oryza sativa (japonica cultivar-group)
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.	AUTHORS	Oryza sativa (japonica cultivar-group)
TITLE	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC clone:OJ118_C02	TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
JOURNAL	Published Only in Database (2001)	JOURNAL	Published Only in Database (2002)
REFERENCE	2 (bases 1 to 95209)	REFERENCE	2 (bases 1 to 187273)
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.	AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE	Direct Submission	TITLE	Direct Submission
COMMENT	Submitted (14-NOV-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)	COMMENT	Submitted (26-NOV-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
FEATURES	Location/Qualifiers	COMMENT	On Jul 27, 2004 this sequence version replaced gi:47971628. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/tdb/glimmer/glimer_form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.
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ORIGIN	Query Match 8.5%; Score 121.6; DB 2; Length 95209; Best Local Similarity 74.0%; Pred. No. 1.7e-17; Matches 188; Conservative 0; Mismatches 49; Indels 17; Gaps 2;	Query Match 8.5%; Score 121.6; DB 2; Length 95209; Best Local Similarity 74.0%; Pred. No. 1.7e-17; Matches 188; Conservative 0; Mismatches 49; Indels 17; Gaps 2;	The orientation of the sequence is from M13 rev to -21M13 of the BAC clone. This sequence of B1047H05 clone has an overlap with P0633B08 (DDBJ: AP003622) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html .
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Qy	755 GAGCTGCAGCTGCTAGAAGCTCCCAACAGACCCCTAGTGTACTCTAGCTGATCGA 814	Qy	755 GAGCTGCAGCTGCTAGAAGCTCCCAACAGACCCCTAGTGTACTCTAGCTGATCGA 814
Db	89049 GAGCTGCAGCTGCTAGAAGCTCCCAACAGACCCCATATGACAACCTACTCTCT 89990	Db	89049 GAGCTGCAGCTGCTAGAAGCTCCCAACAGACCCCATATGACAACCTACTCTCT 89990
Qy	815 TTCACTCTATTTA 828	Qy	815 TTCACTCTATTTA 828

Db	88989 TGGCCTGCAGTAA 88976	Db	88989 TGGCCTGCAGTAA 88976
RESULT	14	RESULT	14
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LOCUS	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, BAC clone:B1047H05.	LOCUS	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, BAC clone:B1047H05.
DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, BAC clone:B1047H05.	DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, BAC clone:B1047H05.
ACCESSION	AP005966	ACCESSION	AP005966
VERSION	AP005966.3	VERSION	AP005966.3
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SOURCE	Oryza sativa (japonica cultivar-group)	SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1	REFERENCE	Oryza sativa (japonica cultivar-group)
AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.	AUTHORS	Oryza sativa (japonica cultivar-group)
TITLE	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC clone:B1047H05	TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
JOURNAL	Published Only in Database (2002)	JOURNAL	Published Only in Database (2002)
REFERENCE	2 (bases 1 to 187273)	REFERENCE	2 (bases 1 to 187273)
AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.	AUTHORS	Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE	Direct Submission	TITLE	Direct Submission
COMMENT	Submitted (26-NOV-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/ , Tel:81-298-38-7441, Fax:81-298-38-7468)	COMMENT	Submitted (26-NOV-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/ , Tel:81-298-38-7441, Fax:81-298-38-7468)
FEATURES	Location/Qualifiers	COMMENT	On Jul 27, 2004 this sequence version replaced gi:47971628. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/tdb/glimmer/glimer_form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.
source	1. . 95209 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="OJ118_C02"	source	A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
ORIGIN	Query Match 8.5%; Score 121.6; DB 2; Length 95209; Best Local Similarity 74.0%; Pred. No. 1.7e-17; Matches 188; Conservative 0; Mismatches 49; Indels 17; Gaps 2;	Query Match 8.5%; Score 121.6; DB 2; Length 95209; Best Local Similarity 74.0%; Pred. No. 1.7e-17; Matches 188; Conservative 0; Mismatches 49; Indels 17; Gaps 2;	The orientation of the sequence is from M13 rev to -21M13 of the BAC clone. This sequence of B1047H05 clone has an overlap with P0633B08 (DDBJ: AP003622) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html .
Db	89109 AGAACATCTGGTAAAGCTGGACTGTGTGGGAGCTCTGACAACCTGGAGATTCTGTGA 754	Db	89109 AGAACATCTGGTAAAGCTGGACTGTGTGGGAGCTCTGACAACCTGGAGATTCTGTGA 89050
Qy	755 GAGCTGCAGCTGCTAGAAGCTCCCAACAGACCCCTAGTGTACTCTAGCTGATCGA 814	Qy	755 GAGCTGCAGCTGCTAGAAGCTCCCAACAGACCCCTAGTGTACTCTAGCTGATCGA 814
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Qy	815 TTCACTCTATTTA 828	Qy	815 TTCACTCTATTTA 828

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 Ehrhartoidea; Oryzeae; Oryza.
 1
 REFERENCE Sasaki,T., Matsumoto,T. and Yamamoto,K.
 AUTHORS TITLE
 JOURNAL Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
 Published Only in Database (2001)
 2 (bases 1 to 134159)
 Sasaki,T., Matsumoto,T. and Yamamoto,K.
 Direct Submission
 Submitted (10-MAY-2001) Takuji Sasaki, National Institute of
 Agrobiological Resources, Rice Genome Research Program; Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
 Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs
 are represented as runs of N. The order of the pieces is believed
 to be correct as given, however the sizes of the gaps between them
 are based on estimates that have provided by the submitter. This
 sequence will be replaced by the finished sequence as soon as it is
 available and the accession number will be preserved.
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 the accession number will be preserved.
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OY      697 ATAAATTAGTAAAGCTGGACTGTT-GGGAGCTCTGTCAAGCCGAGATCTGTGA 754
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 Db 57755 TGGGCTGCAGTTAA 57742

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: September 23, 2005, 12:19:35 ; Search time 577 seconds
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Scoring table: IDENTITY_NUC
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Searched: 4390206 seqs, 2959870657 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

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2: geneseqn1990s:
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5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
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9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	90.4	6.3	2000	12 ADJ41616
8	77.2	5.4	17953	6 AAD38802
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ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	Location/Qualifiers
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FT	TATA_signal				/*tag= C 1247. .2769
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PA	(NOVS)	NOVARTIS AG.		Db	661	ACGTCATTCAGATTCAAATCACAGATTCTTAAAGCTGGACT	720
PA	(NOVS)	NOVARTIS-ERFINDUNGEN VERW GES MBH.					
XK	PT	An G, Jeon J, Chung Y, Lee S;		OY	721	GTTGGGAGCTCTGTCAAGGGAGATTCTGTGAGAAGCTGAGCTGAGCT	780
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DR	P-PSDB; AAY96273.			OY	781	CAACAGACCCCTAGTGTACTCTAGTGTGATGATTCACTCTATTACACCTTG	840
XK	PT	Novel promoters of anther-specific transcription used to create transgenic male-sterile plants.		Db	781	CAACAGACCCCTAGTGTACTCTAGTGTGATGATTCACTCTATTACACCTTG	840
XK	PT	Claim 15; Page 28-29; 32pp; English.		OY	841	TCTCTAGCTATCAAACGTAAGCCAAGCTGAATTAAAGCTTAATGATTGAGT	900
XK	CC	The present sequence is the gene regulator for the rice RAB protein. This protein is expressed in an anther-specific manner in the plant, where it aids in the development of the structure. The gene can be used to create transgenic plants which do not possess a properly formed anther, and thus are male-sterile. This is useful as it prevents self-pollination, which will then aid breeding and hybrid seed production. In addition to rice, this process can also be used in wheat, maize, orchardgrass and sorghum bicolor.		Db	841	TCTCTAGCTATCAAACGTAAGCCAAGCTGAATTAAAGCTTAATGATTGAGT	900
XK	CC	Sequence 1436 BP; 387 A; 313 C; 273 G; 463 T; 0 U; 0 Other;		OY	901	TCTTTTCATCGTAATTCACTTACCGACCTAGTCCGCAATTGAAATTAAATT	960
QY	Query	Best Local Similarity 100.0%; Score 1436; DB 3; Length 1436; Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db	901	TCTTTTCATCGTAATTCACTTACCGACCTAGTCCGCAATTGAAATTAAATT	960
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DY	61	TTCAAAATTGTCTTACAATAAACATTTCCAGCATGAAATCCATACATTAATTTCAG	120	OY	1021	CCTATAAATTATAATTTCAGCGGAGTAAGCATAGTGTATGGTTAATCATCTGG	1080
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OY	481	TTCGTTCCATGTGCGCTCTACGGGGTCACTAGCTGCAAGCTGATGATCGCC	540	RESULT 2			
Db	481	TTCGTTCCATGTGCGCTCTACGGGGTCACTAGCTGCAAGCTGATGATCGCC	540	AAA2733			
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Db	541	AGGATTATTCCTCACATTTCCTATCGCTCTAGCTGCTGTTGGAGCTTA	600	XX	AAA2733;		
OY	601	AAATTATGAAAGCAGCTGCTGAGAAGCTGAGAATTGAGTCT	660	XX	10-AUG-2000 (first entry)		
FH	Key	Location/Qualifiers		XX	Rice RAB anther-specific gene.		

FT	exon	1. .1288	Db	121 CTAATCAGATGCTGGAGCGAAATCTAAGCGATTCAATAGCAAATGATCACTGA
FT	/*tag= e	/number= 1	Qy	181 AGTAACGTGAAAGAGAATATCTCGTTAACATTAGTGCTAGTATTATAACAACTAAA
FT	1. .1196		Qy	240
FT	/*tag= a		Db	181 AGTAACGTGAAAGAGAATATCTCGTTAACATTAGTGCTAGTATTATAACAACTAAA
FT	1116. .1119		Qy	240
FT	/*tag= b		Qy	241 AAATGTTTATTTAGTACAATCGAGTAGCTAGCAGAGCTAGCGTAAGATCG
FT	1145. .1151		Qy	300
FT	/*tag= c		Db	241 AAATGTTTATTTAGTACAATCGAGTAGCTAGCAGAGCTAGCGTAAGATCG
FT	1247. .2769		Qy	300
FT	/*tag= d		Qy	301 TGTTCGGATCACCTGAGAACCGTCAGGGTTGCTGTGCCCTCAGCGATCAGAAT
FT	/product= "RA8"		Db	360
FT	/note= "Contains 2 introns"		Db	360
FT	1289. .1422		Qy	301 TGTTCCGATCACCTGAGAACCGTCAGGGTTGCTGTGCCCTCAGCGATCAGAAT
FT	/*tag= f		Qy	360
FT	/number= 1		Qy	361 TCGGAGATCCGGCGTCTTCTTCTGAAATCTGCAAGTCCCAGCAGCAGCAGCAG
FT	1423. .1555		Db	420
FT	/*tag= g		Db	361 TCGGAGATCCGGCGTCTTCTTCTGAAATCTGCAAGTCCCAGCAGCAGCAGCAG
FT	/number= 2		Qy	421 AGCAAGAGCAATGGCGTGCAAGGGAGTTGATACTTGATGCACTAGCTAGAGCG
FT	1556. .2149		Qy	480
FT	/*tag= h		Db	421 AGCAAGAGCAATGGCGTGCAAGGGAGTTGATACTTGATGCACTAGCTAGAGCG
FT	/number= 2		Db	480
FT	2150. .3003		Qy	481 TTGGTCCATGTCGCTCTACGCCGTGCGAATGTCATGATGATCCTGCATGCATCGCC
FT	/*tag= i		Qy	540
FT	/number= 3		Db	481 TTGGTCCATGTCGCTCTACGCCGTGCGAATGTCATGATGATCCTGCATGCATCGCC
PN	WO200026389-A2.		Qy	540
XX	11-MAY-2000.		Qy	541 AAGATTATTCCTCACATTTCTCTTATCGCTCCTAGTCGTCCTGTTGGAGCTTA
XX	PD		Db	600
XX	02-NOV-1999; 99WO-EP008360.		Qy	541 AAGATTATTCCTCACATTTCTCTTATCGCTCCTAGTCGTCCTGTTGGAGCTTA
XX	PR		Db	600
XX	03-NOV-1998; 98KR-00046973.		Qy	601 AAATTATGAAAGCAGCTGCAAGAGCTAGCTGGTGAAGATTGAGRTCT
PA	(NOVS) NOVARTIS AG.		Db	660
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		Qy	661 ACGTICATTCCAGATTACAATTACAGATCTTAAATTAGTAAAGCTGACT
XX	An G, Jeon J, Chung Y, Lee S;		Db	720
XX	XX		Qy	661 ACGTICATTCCAGATTACAATTACAGATCTTAAATTAGTAAAGCTGACT
DR	WPI; 2000-3655632/31.		Db	720
DR	P-PSDB; AAY96273.		Qy	721 GTTGGAGCTCTGTCAAGCCGGAGATTGTGAGCTGAGCTGAGCTGAGCTCCC
PT	Novel promoters of anther-specific transcription used to create		Db	780
PT	transgenic male-sterile plants.		Qy	721 GTTGGAGCTCTGTCAAGCCGGAGATTGTGAGCTGAGCTGAGCTGAGCTCCC
PS	Claim 3; Page 27-28; 32pp; English.		Db	780
XX	The present sequence is the gene for the rice RAB protein. This protein is expressed in an anther-specific manner in the plant, where it aids in the development of the structure. The gene can be used to create transgenic plants which do not possess a properly formed anther, and thus are male-sterile. This is useful as it prevents self-pollination, which will then aid breeding and hybrid seed production. In addition to rice, this process can also be used in wheat, maize, orchardgrass and Sorghum bicolor.		Qy	781 CAAACAGACCCCTAGTTGACTCTAGCTGATGCGATTCACTCTTATACACCTTG
XX	Sequence 3003 BP; 736 A; 747 C; 694 G; 826 T; 0 U; 0 Other;		Db	840
XX	Best Local Similarity 100.0%; Score 1436; DB 3; Length 3003; Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy	781 CAAACAGACCCCTAGTTGACTCTAGCTGATGCGATTCACTCTTATACACCTTG
Qy	1 CATTCTGAGATCATCTCCAGCCTACATGTTACTCTCCCTATAATACAGTGTCTCTATGA	901	Db	840
Db	1 CATTCTGAGATCATCTCCAGCCTACATGTTACTCTCCCTATAATACAGTGTCTCTATGA	901	Qy	901 TCTTTTCATCGTAATTCACTTACCGAACCTTAGCTGGCATTTGAATTTAAATATT
Qy	61 TTCAAATATTGTCTACATAACATTCCAGCATGAAATCATTAATACAGTGTCTCTATGA	901	Db	960
Db	61 TTCAAATATTGTCTACATAACATTCCAGCATGAAATCATTAATACAGTGTCTCTATGA	901	Qy	961 TTAGAGCTGATTTGATTTTCAAGGGAAATTTCACGTATGTAAGTTTA
Qy	121 CTAATCAGATGCTGGAGCGAAATCTAAGCGATTCAATATGATCACTGA	961	Db	1020
Qy	1021 CCTATAATTAAATTTCAGGGAGTAAGCATAGTTGTTATGGTTATAATCATCTGG	961	Qy	961 TTAGAGCTGATTTGATTTTCAAGGGAAATTTCACGTATGTAAGTTTA
Qy	1021 CCTATAATTAAATTTCAGGGAGTAAGCATAGTTGTTATGGTTATAATCATCTGG	1020	Db	1020
Qy	1081 TATGCTTAATCTCTTACTTGGACTTAGTTGGACAATTCTGTAATGCAATTCTGTC	1081	Qy	1081 TATGCTTAATCTCTTACTTGGACTTAGTTGGACAATTCTGTAATGCAATTCTGTC
Db	1081 TATGCTTAATCTCTTACTTGGACTTAGTTGGACAATTCTGTAATGCAATTCTGTC	1080	Db	1080
Qy	1141 TCTCTATAATACGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	1141	Qy	1141 TCTCTATAATACGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT
Db	1141 TCTCTATAATACGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	1141	Db	1141 TCTCTATAATACGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT
Qy	1201 AGTCCTCAAGGGAAACCGCCTCCATCTCTCCATCCATGGCTCTGCTCTGCTCTG	1201	Qy	1201 AGTCCTCAAGGGAAACCGCCTCCATCTCTCCATCCATGGCTCTGCTCTGCTCTG
Db	1201 AGTCCTCAAGGGAAACCGCCTCCATCTCTCCATCCATGGCTCTGCTCTGCTCTG	1201	Db	1201 AGTCCTCAAGGGAAACCGCCTCCATCTCTCCATCCATGGCTCTGCTCTGCTCTG

QY	1261	CGCCATGCCATGCCATGGCTCTCATGGCAGAGATAACGCAATTAACT	1320	QY	121	CTAACAGATGCTGGAGGAAAATCTAAGCGATTCAATAGCAAAATTGATCACTGA	180
- Db	1261	CGCCATGCCATGCCATGGCTCTCATGGCAGAGATAACGCAATTAACT	1320	Db	121	CTAACAGATGCTGGAGGAAAATCTAAGCGATTCAATAGCAAAATTGATCACTGA	180
QY	1321	TGACGCATATCATCTCATCATCACTTGCAATTCAACTTCTGGATGGCAGAGATTCAGCAATTAACT	1380	QY	181	AGTAAGGAGAATATCTCGTTAACATTGTGATTATTAAACAACTAA	240
- Db	1321	TGACGCATATCATCTCATCATCACTTGCAATTCAACTTCTGGATGGCAGAGATTCAGCAATTAACT	1380	Db	181	AGTAAGGAGAATATCTCGTTAACATTGTGATTATTAAACAACTAA	240
QY	1381	GCTGATCAGTAAACGGTGGCGTGTGAATTGCTCTTATCAGGTGGTCAACCTGG	1436	QY	241	AATATGTTTATTTAGTACAATCAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG	300
- Db	1381	GCTGATCAGTAAACGGTGGCGTGTGAATTGCTCTTATCAGGTGGTCAACCTGG	1436	Db	241	AATATGTTTATTTAGTACAATCAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG	300
RESULT 3				QY	301	TGTTCCGATCACCCTGAGAACCGTCAGGTGGTTGTCCTGCGTCCAGCCGATCAGAAT	360
ID	AAA27335	standard; DNA; 1196 BP.		Db	301	TGTTCCGATCACCCTGAGAACCGTCAGGTGGTTGTCCTGCGTCCAGCCGATCAGAAT	360
XK				QY	361	TCGGAGATCCCGCGTGTCTTCTGAATCTGCAAGTCCACCGCAGCAGCAG	420
AC				Db	361	TCGGAGATCCCGCGTGTCTTCTGAATCTGCAAGTCCACCGCAGCAGCAG	420
XK				DT	10-AUG-2000	(first entry)	
XK				DE		Rice RA8 anther-specific gene promoter.	
KW				KW		RA8; rice; anther-specific; self-pollination; antisense; transgene;	
KW				KW		transgenic plant; wheat; maize; orchardgrass; Sorghum bicolor;	
XK				KW		male-sterile plant; ds.	
OS				XK		Oryza sativa.	
XK				PN	WO2000026389-A2.		
XK				PD	11-MAY-2000.		
XK				PF	02-NOV-1999;	99WO-EP008360.	
XK				PR	03-NOV-1998;	98KR-00046973.	
XK				PR	19-NOV-1998;	98KR-00050126.	
PA				PA	(NOVS) NOVARTIS AG.		
PA				PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XK				PI	An G, Jeon J, Chung Y, Lee S;		
XK				DR	WPI; 2000-365632/31.		
XK				PT	Novel promoters of anther-specific transcription used to create		
PR				PR	transgenic male-sterile plants.		
XK				PS	Claim 9; Page 29; 32pp; English.		
XK				XK	The present sequence is the gene promoter for the rice RA8 protein. This		
CC				CC	protein is expressed in an anther-specific manner in the plant, where it		
CC				CC	aids in the development of the structure. The gene can be used to create		
CC				CC	transgenic plants which do not possess a properly formed anther, and thus		
CC				CC	are male-sterile. This is useful as it prevents self-pollination, which		
CC				CC	will then aid breeding and hybrid seed production. In addition to rice,		
CC				CC	this process can also be used in wheat, maize, orchardgrass and Sorghum		
XK				XK	bicolor.		
SQ		Sequence 1196 BP; 336 A; 242 C; 224 G; 394 T; 0 U; 0 Other;		QY	781	CAAACAGACCCCTAGTTGTAACCTAGCTGATCGATTCACTCTATTATACACCTGG	840
Query Match		83.3%; Score 1196; DB 3; Length 1196;		Db	781	CAAACAGACCCCTAGTTGTAACCTAGCTGATCGATTCACTCTATTATACACCTGG	840
Best Local Similarity		100.0%; Pred. No. 8.9e-290; Matches 1196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		QY	841	TCTCTAGCTTATCAACGTAAGCTGAATTAAAGCTTAATTTGATTTGATGT	900
Matches				Db	841	TCTCTAGCTTATCAACGTAAGCTGAATTAAAGCTTAATTTGATTTGATGT	900
QY	1	CATTCAGAATCATCTCCAGCCTACAACTGTACTCTCCCTAAATACAGTGTCTATGA	60	QY	901	TCTTTCATCGTAATTCACTTACCGACCTAGTCGGATTGAAATTAAATT	960
Db	1	CATTCAGAATCATCTCCAGCCTACAACTGTACTCTCCCTAAATACAGTGTCTATGA	60	Db	901	TCTTTCATCGTAATTCACTTACCGACCTAGTCGGATTGAAATTAAATT	960
QY	61	TTCAAAATTGTCTTACAAATAACATTCCAGCATGAAATCCATTAAATTTCAG	120	QY	961	TTAGAGCTGATTGATTTTCAGCGGAATTTCAGTATGTAAGTTTA	1020
Db	61	TTCAAAATTGTCTTACAAATAACATTCCAGCATGAAATCCATTAAATTTCAG	120	Db	961	TTAGAGCTGATTGATTTTCAGCGGAATTTCAGTATGTAAGTTTA	1020
QY	1021	CCTTAAATTAAATTTCAGCGGAATTTCAGTATGTTATGCAATTACATCTGG	1080	QY	1081	TATGTTAACTCTTACTGGACTTAGTGGCAATTCTGTAATGCAATTCTCGTGC	1140
Db	1021	CCTTAAATTAAATTTCAGCGGAATTTCAGTATGTTATGCAATTACATCTGG	1080	Db	1081	TATGTTAACTCTTACTGGACTTAGTGGCAATTCTGTAATGCAATTCTCGTGC	1140
QY	1141	TCTCTATAATACGGCCTGCTAGCTTGTCTTGTATCTGCAACAGACTAGCTG	1196	QY	1141	TCTCTATAATACGGCCTGCTAGCTTGTCTTGTATCTGCAACAGACTAGCTG	1196
Db	1141	TCTCTATAATACGGCCTGCTAGCTTGTCTTGTATCTGCAACAGACTAGCTG	1196	Db			

RESULT 4

AAA27341 standard; DNA; 240 BP.

ID AAA27341;

XX DT 10-AUG-2000 (first entry)

XX DE Rice RAB anther-specific gene fragment.

KW RAB; rice; anther-specific; self-pollination; antisense; transgene; male-sterile plant; ds.

XX OS Oryza sativa.

XX FH Key Location/Qualifiers

FT exon 1. .92

FT FT /*tag= b

FT /number= 1

FT CDS 51. .240

FT FT /*tag= a

FT FT /*product= "RAB"

FT FT /note= "Contains an intron"

FT FT 93. .226

FT FT /*tag= c

FT FT /number= 1

FT FT 227. .240

FT FT /*tag= d

FT FT /number= 2

XX PN WO200026389-A2.

XX PD 11-MAY-2000.

XX PR 02-NOV-1999; 99WO-EP008360.

XX PR 03-NOV-1998; 98KR-00046973.

XX PR 19-NOV-1998; 98KR-00050126.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI An G, Jeon J, Chung Y, Lee S;

XX DR WPI; 2000-365632/31.

DR P-PSDB; AAY96273.

XX PT Novel promoters of anther-specific transcription used to create transgenic male-sterile plants.

XX PS Claim 13; Page 32; 32pp; English.

The present sequence is part of the gene for the rice RAB protein. This protein is expressed in an anther-specific manner in the plant, where it aids in the development of the structure. The gene can be used to create transgenic plants which do not possess a properly formed anther, and thus are male-sterile. This is useful as it prevents self-pollination, which will then aid breeding and hybrid seed production. In addition to rice, this process can also be used in wheat, maize, orchardgrass and Sorghum bicolor. This sequence was used to create an expression vector for the protein.

Sequence 240 BP; 51 A; 71 C; 49 G; 69 T; 0 U; 0 Other;

Query Match 16.7%; Score 240; DB 3; Length 240;

Best Local Similarity 100.0%; Pred. No. 4.6e-50;

Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC The present sequence is the gene for the rice RAB protein. This protein is expressed in an anther-specific manner in the plant, where it aids in the development of the structure. The gene can be used to create transgenic plants which do not possess a properly formed anther, and thus are male-sterile. This is useful as it prevents self-pollination, which will then aid breeding and hybrid seed production. In addition to rice, this process can also be used in wheat, maize, orchardgrass and Sorghum bicolor.

CC Sequence 1008 BP; 145 A; 360 C; 325 G; 178 T; 0 U; 0 Other;

CC Query Match 6.6%; Score 95; DB 3; Length 1008;

CC Best Local Similarity 100.0%; Pred. No. 2e-13;

CC Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sequence 1008 BP; 145 A; 360 C; 325 G; 178 T; 0 U; 0 Other;

CC Query Match 1197 GCAAAGTCTCAAGGGAAACGCCCTCATCTCTCAGCTCCATGCTCCATGGCTCCC 1256

CC 1 GCAAAGTCTCAAGGGAAACGCCCTCATCTCTCAGCTCCATGGCTCCC 60

QY 1257 TCGTGCCTGCCATGCCATGGCTTCATGGCGAGAGATCCAGCATGCTGAATT 1316

Db 61 TCGTGCCTGCCATGCCATGGCTTCATGGCGAGAGATCCAGCATGCTGAATT 120

QY 1317 AACTTGACGCATATCATCTCATCATCACTTGATTCACITCTGGATTTGCGAGACATG 1376

Db 121 AACTTGACGCATATCATCTCATCACTTGATTCACITCTGGATTTGCGAGACATG 180

QY 1377 TTAGCTGATCAGTAACGTTGCCGTGTTGAATGGTCTTATCAGGGTTCAACCTGG 1436

Db 181 TTAGCTGATCAGTAACGTTGCCGTGTTGAATGGTCTTATCAGGGTTCAACCTGG 240

RESULT 5

AAA27338

ID AAA27338 standard; cDNA; 1008 BP.

XX AC AAA27338;

XX DT 10-AUG-2000 (first entry)

XX DE Rice RAB anther-specific gene.

XX RA8; rice; anther-specific; self-pollination; antisense; transgene; KW transgenic plant; wheat; maize; orchardgrass; Sorghum bicolor; KW male-sterile plant; ss.

XX OS Oryza sativa.

XX FH Key Location/Qualifiers

FT CDS 51. .845

FT FT /*tag= a

FT FT /*product= "RAB"

FT FT /note= "Contains an intron"

FT FT 98KR-00046973.

FT FT 19-NOV-1998; 98KR-00050126.

XX PN WO200026389-A2.

XX PD 11-MAY-2000.

XX PR 02-NOV-1999; 99WO-EP008360.

XX PR 03-NOV-1998; 98KR-00046973.

XX PR 19-NOV-1998; 98KR-00050126.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI An G, Jeon J, Chung Y, Lee S;

XX DR WPI; 2000-365632/31.

DR P-PSDB; AAY96273.

XX PT Novel promoters of anther-specific transcription used to create transgenic male-sterile plants.

XX PS Claim 19; Page 31; 32pp; English.

The present sequence is the gene for the rice RAB protein. This protein is expressed in an anther-specific manner in the plant, where it aids in the development of the structure. The gene can be used to create transgenic plants which do not possess a properly formed anther, and thus are male-sterile. This is useful as it prevents self-pollination, which will then aid breeding and hybrid seed production. In addition to rice, this process can also be used in wheat, maize, orchardgrass and Sorghum bicolor.

Qy	1257 TCGTCGCCATGCCATGGCTCATGGTG 1291	Db	1 GCAAAAGCCTCAAAGGCGAACCCGCCTCCATCTCCTCCATGGCGTCCC 60
Qy	61 TCGTCGCCATGCCATGGCTCATGGTG 95	Db	1866 AAGATGCAACTGCTAAAACCTCCCTTAATAGGTCCRT 1903
RESULT 6		RESULT 7	
ADA71441		ADJ41616	
ID ADA71441 standard; DNA; 2000 BP.		ID ADJ41616 standard; cDNA; 2000 BP.	
XX		XX	
AC ADA71441;		AC ADJ41616;	
XX		XX	
DT 20-NOV- 2003 (first entry)		DT 06-MAY-2004 (first entry)	
XX		XX	
DB Rice gene, SEQ ID 4764.		DB Plant CDNA #2616.	
XX		XX	
KW Plant; bacterial infection; fungal infection; viral infection; rice; gene; db.		KW Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral; antifungal.	
XX		XX	
OS Oryza sativa.		OS Bukaryota.	
XX		XX	
PN WO2003000898-A1.		PN US2004016025-A1.	
XX		XX	
PD 03-JAN-2003.		PD 22-JAN-2004.	
XX		XX	
PF 22-JUN-2001; 2001WO-IB001105.		PF 26-SEP-2002; 2002US-00260238.	
XX		XX	
PR 22-JUN-2001; 2001WO-IB001105.		PR 26-SEP-2001; 2001US-0325277P.	
XX		PR 26-SEP-2001; 2001US-0325448P.	
PA (SYGN) SYNGENTA PARTICIPATIONS AG.		PR 04-APR-2002; 2002US-0370620P.	
XX		XX	
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y; Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; DR WPI; 2003-175290/17.		PA (BUDW/) BUDWORTH P. (MOUG/) MOUGHAMER T. (BRIG/) BRIGGS S P. (COOP/) COOPER B. (GLAZ/) GLAZE BROOK J. (GOFF/) GOFF S A. (KATA/) KATAGIRI F. (KREP/) KREPS J. (PROV/) PROVART N. (RICK/) RICKE D. (ZHUT/) ZHU T.	
XX		XX	
CC The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.		CC Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F, Kreps J, Provar N, Riche D, Zhu T; DR WPI; 2004-190374/18.	
CC Sequence 2000 BP; 630 A; 343 C; 386 G; 640 T; 0 U; 1 Other;		XX New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.	
SQ		XX Claim 1; SEQ ID NO 2616; 230pp; English.	
Query Match 6.3%; Score 90.4; DB 8; Length 2000;		XX Claim 1; SEQ ID NO 2616; 230pp; English.	
Best Local Similarity 71.1%; Pred. No. 3.8e-12;		CC The invention relates to plant nucleotide sequences that direct seed-leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism,	
Matches 155; Conservative 0; Mismatches 46; Indels 17; Gaps 2;		CC Qy 593 GGAGCTTAAATTATGAAAGCAGCTGCTGAGAATCTGAAGAATT 652	
Db 1686 GGAGCTTAAAGTTCTGAGAAGCAACTGCTAGCTGGTAGAGAAC 1745		CC Qy 653 TGAGTCTAC-----GTTCATCTCCAGATCTACAATTACAGATTCA 697	
Db 1746 TGAGAACCCAGCTCTGCTCTAGTTCCAGATCTACATCTAGATTCA 1805		CC Qy 698 TAATTAGGTAAAAGCTGGACTGTTGG-GAGCTCTGTCAGCCGGAGATCTGTGAG 755	
Db 1806 GAATCTTGTTAAAGATGGGTTGGTAGGGAGCTTGTAGAGATTAGGAG 1865		CC Qy 1806 GAATCTTGTTAAAGATGGGTTGGTAGGGAGCTTGTAGAGATTAGGAG 1865	

CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX sequence 2000 BP; 628 A; 343 C; 387 G; 641 T; 0 U; 1 Other;
 SQ

Query Match	Score	DB	Length
Best Local Similarity	6.3%	12	2000
Matches	155		
Conservative	0		
Mismatches	46		
Indels	17		
Gaps	2		

QY 593 GGAGCTTAAATTATGAAAAGCAGCTGCTGAGAAGCTACCTGGTGAAGAATCTGAGAATT 652
 DB 1688 GGAGCTTAAGATTCTGAGAAGCACTGCTAAGAAGCTAGCTGGTGAAGAATCTGAGAAGC 1747
 QY 653 TGTGTTCTAC-----GTTCATCTCCAGATTCTACAATTACAGATTCTA 697
 DB 1748 TGGAAACCCAGCTCTGCTCTAGTCATTTCAGATTCTACATCTATAAGATTCTTA 1807
 QY 698 TAATTAGTAGGAAAAGCTGACTGTGTTGG--GAGCTCTCTAGCCGAGATCTGTGAG 755
 DB 1808 GAATCTGGTAAAGATGGGTGTTAGGGAGAGCTTGTAGCTAGAGATTAGGAG 1867
 QY 756 AAGCTGCAGCTGCTAGAAGCTCCCCAACAGACCCCT 793
 DB 1868 AAGATGCAACTGCTTAAACTCCTTAATAAGTCCTT 1905

RESULT 8

ID	Accession	Description	Length
AAD38802	AAD38802	standard; DNA; 17953 BP.	17953
XK			
AC			
XX			
DT			
XX			
DE			
Rice RGAB contig.3ONippon DNA.			

Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene; KW AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; KW resistance; agricultural; horticultural; plant protectant; ds. KW Oryza sativa. KW WO200234927-A2. KW 02-MAY-2002. KW 19-OCT-2001; 2001WO-US046331. KW 20-OCT-2000; 2000US-0242313P. PR 09-JUL-2001; 2001US-0303897P. XX (WISC) WISCONSIN ALUMNI RES FOUND. PA (USDA) US DEPT OF AGRICULTURE. XX PI Leong SA, Farman ML, Chauhan RS, Durfee TJ; DR WPI; 2002-471442/50. XX New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39. XX Example 2; Page 59-68; 175pp; English.

PS

XX The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-

CC co39(t) nucleic acids may be used as probes to detect the presence of CC and/or expression of Pi-CO39(t) genes, and to produce large quantities of CC pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful CC in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t) CC polypeptides. The transgenic plants are useful for plant breeding or CC directly in agricultural or horticultural applications. The present sequence is rice RGAB contig.3ONippon DNA. This sequence comprises CC portion of BAC clone 82N20 from Nipponbare, containing RGAB sequence and CC ORF NBR7

SQ Sequence 17953 BP; 5074 A; 3615 C; 3742 G; 5522 T; 0 U; 0 Other;

Query Match	Score	DB	Length
Best Local Similarity	5.4%	6	17953
Matches	142		
Conservative	0		
Mismatches	53		
Indels	13		
Gaps	2		

QY 589 TTTGGGAGCTTAAATTATGAAAAGCAGCTGCTGAGAAGCTAGCTGGTGAAG 648
 DB 17088 TTGGGAGCTTAAAGATCTCTAGCTGAGATCTGCTGAGCTGCTGCTGATAATCTGGAA 17147
 QY 649 AATTGAGRTCTACGTTCTCCAGATTCTACAAATTACAGATTCTTATAATTAGCTA 708
 DB 17148 AAGTGGRTT---TTCACCTCTGGCTTCTAACTACAGATTCTTGAACCTGAGTG 17203
 QY 709 AAAAGCTGACTGTTGGGAGCTCTGTCAGCCCCAGATTCTGTGAGAAGCTGCAGCTGC 768
 DB 17204 AGAATGTTAGACTATTGAGG-----AGCTGGAATTCTAAAGAAGACTGCAATAAC 17254
 QY 769 TAGAGCTTCCCCAACAGACCCCTAGT 796
 DB 17255 TAGAGCTCACTCAAACAGGCCCTAGT 17282

RESULT 9

ID	Accession	Description	Length
ADA72788/C	ADA72788	standard; DNA; 2000 BP.	2000
XX			
AC			
XX			
DT			
XX			
DE			
Rice gene, SEQ ID 6113.			
XX			
KW			
Plant; bacterial infection; fungal infection; viral infection; rice; KW gene; ds.			
XX			
OS			
XX			
PN			
XX			
PD			
XX			
PF			
XX			
PR 03-JAN-2003.			
XX			
22-JUN-2001; 2001WO-IB001105.			
XX			
(SYGN) SYNGENTA PARTICIPATIONS AG.			
XX			
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y; PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G; DR WPI; 2003-175290/17.			
XX			
Identifying at least one gene involved in plant resistance or response to PT pathogenic infection for conferring resistance or tolerance to a plant to PT bacterial, fungal or viral infection by determining or detecting plant PT gene expression.			
XX Claim 27; SEQ ID NO 6113; 899pp; English.			
CC The present invention relates to a method (M1) for identifying genes CC involved in plant resistance or response to pathogenic infection. M1 CC			

CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

XX Sequence 2000 BP; 497 A; 452 C; 457 G; 594 T; 0 U; 0 Other;

SQ Query Match 4.9%; Score 71; DB 8; Length 2000;
 Best Local Similarity 66.4%; Pred. No. 2.8e-07; Mismatches 50; Indels 23; Gaps 2;
 Matches 144; Conservative 0; Mismatches 50; Indels 23; Gaps 2;
 QY 589 TTGGGAGCTAAATTATGAAAGCAGCTGCTGAGAACGACTGAGAATCTGAG 648
 Db 859 TTGGGAGCTAAATTATGAAAGCAGCTGCTGAGAACGACTGAGAATCTGAGA 800
 QY 649 ATTTGAGTCTACG-----TTCAATTCTCAGATTCTACAAATTACAGATT 693
 Db 799 AAGTAGATTTCCAACATTATGGCTCTATTATTTCTAGATTCTACAACTAGTT 740
 QY 694 CTATAATTAGGTAAAAGCTGGACTGTTGGAGCTCTGTCAAGCCGAGATCTGTG 753
 Db 739 CTAGAACTCTAGACCAAAGCTGAACCTGTTAGGAATTCT-----AATCTAGG 688
 QY 754 AGAAGCTGCACTGCAGCTGCTAGAACAGACC 790
 Db 687 AGAACGCTGCTGCAACTCCCCAACAGACC 651

RESULT 10
 ADA72600/C
 ID ADA72600 Standard; DNA; 2000 BP.
 XX AC ADA72600;
 XX DT 20-NOV-2003 (first entry)
 XX DE Rice gene, SEQ ID 5925.
 XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
 XX KW gene; ds.
 XX OS Oryza sativa.
 XX PN WO2003000898-A1.
 XX PR 03-JAN-2003.
 XX PD 22-JUN-2001; 2001WO-IB001105.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX DR WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX PS Claim 27; SEQ ID NO 5925; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 the incompatible interaction of plant gene expression relative to
 expression of the gene in an uninfected plant, in a mutant plant that
 does not express a gene associated with response to pathogenic infection,
 or in a corresponding incompatible or compatible interaction. (M1) is
 useful for conferring resistance to resistance or tolerance to a plant to
 bacterial, fungal or viral infection. The present sequence was used to
 illustrate the invention.

CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 the incompatible interaction of plant gene expression relative to
 expression of the gene in an uninfected plant, in a mutant plant that
 does not express a gene associated with response to pathogenic infection,
 or in a corresponding incompatible or compatible interaction. (M1) is
 useful for conferring resistance to resistance or tolerance to a plant to
 bacterial, fungal or viral infection. The present sequence was used to
 illustrate the invention.

CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

XX Sequence 2000 BP; 617 A; 367 C; 428 G; 586 T; 0 U; 2 Other;

SQ Query Match 4.8%; Score 69.2; DB 8; Length 2000;
 Best Local Similarity 76.6%; Pred. No. 7.9e-07; Mismatches 28; Indels 2; Gaps 1;
 Matches 98; Conservative 0; Mismatches 28; Indels 2; Gaps 1;
 QY 664 TTCATTCTCCAGATTCTACAGATTCTTAATTAGTAAAGCTGGACTGTT 723
 Db 985 TTATTTTCGATTCTACACTACCGATTCTCAGAATCTGGTAAATAACTGTT 926
 QY 724 T-GGGAGCTCTGTCAGCCGAGATTCGTGAGAACGCTGAGCTCCC 781
 Db 925 TGAGGGAGTTCTAGCAGCTGGAGATTCTACAGAGCTGAGCTGCCCT 866
 QY 782 AACAGAC 789
 Db 865 AAATAGGC 858

RESULT 11

ADA71536
 ID ADA71536 Standard; DNA; 2000 BP.
 XX AC ADA71536;
 XX DT 20-NOV-2003 (first entry)
 XX DE Rice gene, SEQ ID 4859.
 XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
 XX KW gene; ds.
 XX OS Oryza sativa.
 XX PN WO2003000898-A1.
 XX PR 03-JAN-2003.
 XX PD 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX DR WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX PS Claim 27; SEQ ID NO 4859; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 the incompatible interaction of plant gene expression relative to
 expression of the gene in an uninfected plant, in a mutant plant that
 does not express a gene associated with response to pathogenic infection,
 or in a corresponding incompatible or compatible interaction. (M1) is
 useful for conferring resistance to resistance or tolerance to a plant to
 bacterial, fungal or viral infection. The present sequence was used to
 illustrate the invention.

XX SQ Sequence 2000 BP; 653 A; 376 C; 363 G; 607 T; 0 U; 1 Other;

Query Match 4.2%; Score 60.4; DB 8; Length 2000;
Best Local Similarity 62.5%; Pred. No. 0.00013; Mismatches 53; Indels 23; Gaps 1;
Matches 115; Conservative 0; Mismatches 61; Indels 8; Gaps 1;

QY 608 GAAAGCAGCTGCTGAGAAGCTAGCTGGTGAAGAATCTGAGAATTGAGTTGAGTCTACGTCA 667
200 GTAAACCCAGTTCTGAGAATCTGAGATAAGCTGCTGGCTTCAGTTCTGGCTCTAGTACA 259

QY 668 TTTCTCCAGATTCTACATTACAGATTCTATTAGTAAAGCTGAGCTGGACTGTTGGG 727
260 TTTCTCGGATTCTACAACATAACTCTTAGAACCTGAACTAACGTAATGGTGGG 319

QY 728 AGCTTCCTGTCAGCCGGAGATTCTGAGAAGCTGCAGCTGCTAGAACCAAAGCTAAATGGTGGG 787
320 ATAGTTCT-----GATTATGGGAGACTGCAAGCTGAGCTAACACTCTCCAAACAG 371

QY 788 ACCC 791
Db 372 GCCC 375

RESULT 12
ADA73357/C

ID ADA73357 standard; DNA; 2000 BP.

XX AC ADA73357;
XX DT 20-NOV-2003 (first entry)

DE Rice gene, SEQ ID 6683.

XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
OS Oryza sativa.
XX PN WO2003000898-A1.
XX PD 03-JAN-2003.
XX PF 22-JUN-2001; 2001WO-1B001105.
XX PR 22-JUN-2001; 2001WO-1B001105.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y, Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, zhu T, zou G;
DR WPI; 2003-175290/17.

XX PT Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX PS Claim 27; SEQ ID NO 6683; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

XX Sequence 2000 BP; 618 A; 438 C; 283 G; 660 T; 0 U; 1 Other;

XX SQ Sequence 2000 BP; 653 A; 376 C; 363 G; 607 T; 0 U; 1 Other;

Query Match 4.1%; Score 59.2; DB 8; Length 2000;
Best Local Similarity 63.8%; Pred. No. 0.00026; Mismatches 53; Indels 23; Gaps 2;
Matches 134; Conservative 0; Mismatches 53; Indels 23; Gaps 2;

QY 590 TTGGGAGCTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAAGAATCTGAGA 649
Db 1592 TTGGGAGCTAAATTATGAAAGCAGCTGCTGCTGAGAATCTGAGAATATGGAAA 1533

QY 650 ATTGAGTTCTAC-----GTCATTCTCCAGATTCTACAAATACAGATTC 694
Db 1532 AGCTGGTTCTGCCTCTGGTGTAGTTATTITGATTTGAGTTAACTACAGATTC 1473

QY 695 TTATAATTAGTAAAGCTGAGCTGTTGGAGCTCTGTCAAGCCGGAGATTCGTGA 754
Db 1472 TCAGAATCTGGGTGATAATCTGGACTGTTGAGAG-----AACTGGAGATTCTGGTA 1421

QY 755 GAAGCTGCAGCTGCTAGAACGTTCCCAA 784
Db 1420 AAATCTGCCAACACTAGAACAAATCCCCCAA 1391

RESULT 13
ADJ40892

ID ADJ40892 standard; cDNA; 2000 BP.

XX AC ADJ40892;
XX DT 06-MAY-2004 (first entry)

DE Plant CDNA #1892.

XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antifungal; antiviral; antifungal.

XX OS Eukaryota.

XX PN US2004016025-A1.

XX PD 22-JAN-2004.

XX PR 26-SEP-2002; 2002US-00260238.

XX PR 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

XX PI Budworth P, Moughamer T, Briggs S P, Cooper B, Glazebrook J, Goff S A, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX DR WPI; 2004-190374/18.

XX PT New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.

PS Claim 33; SEQ ID NO 1892; 230pp; English.

XX
CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

Query Match 4.1%; Score 58.8; DB 12; Length 2000;
 Best Local Similarity 66.5%; Pred. No. 0.00032;
 Matches 141; Conservative 0; Mismatches 47; Indels 24; Gaps 3

Oy 589 TTTGGGAGCTTAAATTATGAAAGCAGCTGCTGAGAAGCTAGCTCGTGAGAATCTGAAG 648

RESULT 14
ADD38805/C

ID AAD38805 standard; DNA; 11460 BP.
XX
AC

23-SEP-2002 (first entry)
DT
XX

XX
KW Rice; chromosome 11; Indica rice cultivar; c039; avirulence gene;

KW resistance; agricultural; horticultural; plant protectant; ds. XX OS *Canna sativa*

XX
PN WO200234927-A2.

PD
XX
02-MAY-2002.

XX

XX
PA
(WISC) WISCONSIN ALUMNI BES FORMER

XX
PA
USDA) US DEPT OF AGRICULTURE.

DR
XX
PT New PIC039(t) polynucleotides from chromosome 11 of Indica rice cultivar
PT CO39 useful for conferring or improving resistance of plants to strains
PT of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-
PT CO39.
XX
PS Claim 6; Page 143-148; 175pp; English.
XX
CC The invention relates to a polynucleotide isolated from chromosome 11 of
CC Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising
CC one or more genes that confer resistance to strains of Magnaporthe grisea
CC having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are
CC useful for conferring or improving resistance of plants to strains of the
CC rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-
CO39(t) nucleic acids may be used as probes to detect the presence of
CC and/or expression of Pi-CO39(t) genes, and to produce large quantities of
pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful
CC in producing polyclonal or monoclonal antibodies useful as sensitive
CC detection reagents for the presence and accumulation of Pi-CO39(t)
CC polypeptides. The transgenic plants are useful for plant breeding or
CC directly in agricultural or horticultural applications. The present
CC sequence is CODRI ORF from rice variety CO39
XX
SQ Sequence 11460 BP; 3238 A; 2381 C; 2138 G; 3703 T; 0 U; 0 Other;

XX
DR
XX
WPI; 2002-471442/50.

PT New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39.

XX

PS Example 4; Page 110-142; 175pp; English.

XX
CC The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-CO39(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-CO39(t) genes, and to produce large quantities of pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t) polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or horticultural applications. The present sequence is BAC clone E2P5 from rice variety CO39

XX

SQ Sequence 69300 BP; 19720 A; 15094 C; 15006 G; 19380 T; 0 U; 100 Other;

Query Match 4.0%; Score 57.6; DB 6; Length 69300;
Best Local Similarity 63.0%; Pred. No. 0.0026; Mismatches 56; Indels 8; Gaps 1;
Matches 109; Conservative 0;

Qy	638	AGAATCTGAGAAATTGAGTTCACTCGTTCAGATTCTACATACTACAGATTCTTA	697
Db	12015	ACGCTTCTCCAGCTTCTGGCTTCTTAGTTCTCAGATTCTGTACTACAGATTCTCA	12074
Qy	698	TATTTAGGTTAAAAGCTGGACTGTTGGAGCTCTGTCAGCCGGAGATTCTGTGAGAA	757
Db	12075	GAAGCTGTGGACTG-----TTGGGGTAGCTCTAGCAGAACGCCTTTGGAAA	12126
Qy	758	GCTGCAGCTGCTAGAAGCTCCCCAACAGACCCCTAGTGTACTCTAGCTGA	810
Db	12127	GTACAGCTGGACACGCTCCCAACAGGACCTAAGTTACACAGTTGGTCA	12179

Search completed: September 23, 2005, 17:11:19
Job time : 583 secs

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